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Description

This invention relates to plant cells and plants, the genomes of which are transformed to contain at least two genes, each coding for a different non-competitively binding Bacillus thuringiensis ("B. thuringiensis" or "Bt") insecticidal crystal protein ("ICP") for a specific target insect species, preferably belonging to the order of Lepidoptera or Coleoptera. Such transformed plants have advantages over plants transformed with a single B. thuringiensis ICP gene, especially with respect to the prevention of resistance development in the target insect species against the at least two B. thuringiensis ICPs, expressed in such plants.

This invention also relates to a process for the production of such transgenic plants, taking into account the competitive and non-competitive binding properties of the at least two B. thuringiensis ICPs in the target insect species' midgut. Simultaneous expression in plants of the at least two genes, each coding for a different non-competitively binding B. thuringiensis ICP in plants, is particularly useful to prevent or delay resistance development of insects against the at least two B. thuringiensis ICPs expressed in the plants.

This invention further relates to a process for the construction of novel plant expression vectors and to the novel plant expression vectors themselves, which contain the at least two B. thuringiensis ICP genes encoding the at least two non-competitively binding B. thuringiensis ICPs. Such vectors allow integration and coordinate expression of the at least two B. thuringiensis ICP genes in plants.

BACKGROUND OF THE INVENTION

Since the development and the widespread use of chemical insecticides, the occurrence of resistant insect strains has been an important problem. Development of insecticide resistance is a phenomenon dependent on biochemical, physiological, genetic and ecological mechanisms. Currently, insect resistance has been reported against all major classes of chemical insecticides including chlorinated hydrocarbons, organophosphates, carbamates, and pyrethroid compounds (Brattsten et al., 1986).

In contrast to the rapid development of insect resistance to synthetic insecticides, development of insect resistance to bacterial insecticides such as B. thuringiensis sprays has evolved slowly despite many years of use (Brattsten et al., 1986). The spore forming gram-positive bacterium B. thuringiensis produces a parasporal crystal which is composed of crystal proteins (ICPs) having insecticidal activity. Important factors decreasing the probability of emergence of resistant insect strains in the field against B. thuringiensis sprays are: firstly the short half-life of B. thuringiensis sprays after foliar application; secondly the fact that commercial B. thuringiensis preparations often consist of a mixture of several insecticidal factors including spores, ICPs and eventually beta-exotoxins (Shields, 1987); and thirdly the transitory nature of plant-pest interactions. Many successful field trials have shown that commercial preparations of a B. thuringiensis containing its spore-crystal complex, effectively control lepidopterous pests in agriculture and forestry (Krieg and Langenbruch, 1981). B. thuringiensis is at present the most widely used pathogen for microbial control of insect pests.

Various laboratory studies, in which selection against B. thuringiensis was applied over several generations of insects, have confirmed that resistance against B. thuringiensis is seldom obtained. However, it should be emphasized that the laboratory conditions represented rather low selection pressure conditions.

For example, Goldman et al. (1986) have applied selection with B. thuringiensis israelensis toxin over 14 generations of Aedes aegypti and found only a marginal decrease in sensitivity. The lack of any observable trend toward decreasing susceptibility in the selected strains may be a reflection of the low selection pressure (LC₅₀) carried out over a limited number of generations. However, it should be pointed out that Georgiou et al. (In : Insecticide Resistance in Mosquitoes : Research on new chemicals and techniques for management. In "Mosquito Control Research, Annual Report 1983, University of California.") with Culex quinquefasciatus obtained an 11-fold increase in resistance to B. thuringiensis israelensis after 32 generations at LC₉₅ selection pressure.

McGaughey (1985) reported that the grain storage pest Plodia interpunctella developed resistance to the spore-crystal complex of B. thuringiensis; after 15 generations of selection with the Indian meal moth, Plodia interpunctella, using a commercial B. thuringiensis HD-1 preparation ("Dipel", Abbott Laboratories, North Chicago, Illinois 60064, USA), a 100-fold decrease in B. thuringiensis sensitivity was reported. Each of the colonies was cultured for several generations on a diet treated with a constant B. thuringiensis dosage which was expected to produce 70-90% larval mortality. Under these high selection pressure conditions, insect resistance to B. thuringiensis increased rapidly. More recently, development of resistance against B. thuringiensis is also reported for the almond moth, Cadra cautella (McGaughey and Beeman, 1988). Resistance was stable when selection was discontinued and was inherited as a recessive trait (McGaughey and Beeman, 1988). The mechanism of insect resistance to B. thuringiensis toxins of Plodia interpunctella and Cadra cautella has not been elucidated.

The main cause of *B. thuringiensis* resistance development in both reported cases involving grain storage was the environmental conditions prevailing during the grain storage. Under the conditions in both cases, the environment was relatively stable, so *B. thuringiensis* degradation was slow and permitted successive generations of the pest to breed in the continuous presence of the microbial insecticide. The speed at which *Plodia* developed resistance to *B. thuringiensis* in one study suggests that it could do so within one single storage season in the bins of treated grain.

Although insect resistance development against *B. thuringiensis* has mostly been observed in laboratory and pilot scale studies, very recent indications of *B. thuringiensis* resistance development in *Plutella xylostella* populations in the (cabbage) field have been reported (Kirsch and Schmutterer, 1988). A number of factors have led to a continuous exposure of *P. xylostella* to *B. thuringiensis* in a relatively small geographic area. This and the short generation cycle of *P. xylostella* have seemingly led to an enormous selection pressure resulting in decreased susceptibility and increased resistance to *B. thuringiensis*.

A procedure for expressing a *B. thuringiensis* ICP gene in plants in order to render the plants insect-resistant (European patent publication ("EP") 0193259 Vaeck et al., 1987; Barton et al., 1987; Fischhoff et al., 1987) provides an entirely new approach to insect control in agriculture which is at the same time safe, environmentally attractive and cost-effective. An important determinant for the success of this approach will be whether insects will be able to develop resistance to *B. thuringiensis* ICPs expressed in transgenic plants (Vaeck et al., 1987; Barton et al., 1987; Fischhoff et al., 1987). In contrast with a foliar application, after which *B. thuringiensis* ICPs are rapidly degraded, the transgenic plants will exert a continuous selection pressure. It is clear from laboratory selection experiments that a continuous selection pressure has led to adaptation to *B. thuringiensis* and its components in several insect species. In this regard, it should be pointed out that the conditions in the laboratory which resulted in the development of insect-resistance to *B. thuringiensis* are very similar to the situation with transgenic plants which produce *B. thuringiensis* ICPs and provide a continuous selection pressure on insect populations feeding on the plants. Mathematical models of selection pressure predict that, if engineered insect-resistant plants become a permanent part of their environment, resistance development in insects will emerge rapidly (Gould, 1988). Thus, the chances for the development of insect resistance to *B. thuringiensis* in transgenic plants may be considerably increased as compared to the field application of *B. thuringiensis* sprays. A *Heliothis virescens* strain has been reported that is 20 times more resistant to *B. thuringiensis* HD-1 ICP produced by transgenic *Pseudomonas fluorescens* and 6 times more resistant to the pure ICP (Stone et al., 1989). Furthermore, the monetary and human costs of resistance are difficult to assess, but loss of pesticide effectiveness invariably entails increased application frequencies and dosages and, finally, more expensive replacement compounds as new pesticides become more difficult to discover and develop.

Therefore, it would be desirable to develop means for delaying or even preventing the evolution of resistance to *B. thuringiensis*.

B. thuringiensis strains, active against Lepidoptera (Dulmage et al., 1981), Diptera (Goldberg and Margalit, 1977) and Coleoptera (Krieg et al., 1983), have been described. It has become clear that there is a substantial heterogeneity among ICPs from different strains active against Lepidoptera, as well as among ICPs from strains active against Coleoptera (Hofte and Whiteley, 1989). An overview of the different *B. thuringiensis* ICP genes, that have been characterized, is given in Table 2 (which follows the Examples herein).

Most of the anti-Lepidopteran *B. thuringiensis* (e.g., Bt3, Bt2, Bt73, Bt14, Bt15, Bt4, Bt18) ICP genes encode 130 to 140 kDa protoxins which dissolve in the alkaline environment of an insect's midgut and are proteolytically activated into an active toxin of 60-65 kDa. These ICPs are related and can be recognized as members of the same family based on sequence homologies. The sequence divergence however is substantial, and the insecticidal spectrum, among the order Lepidoptera, may be substantially different (Höfte et al., 1988).

The P2 toxin gene and the cry B2 gene are different from the above-mentioned genes in that they do not encode high molecular weight protoxins but rather toxins of around 70 kDa (Donovan et al., 1988 and Widner and Whiteley, 1989, respectively).

It has recently become clear that heterogeneity exists also in the anti-Coleopteran toxin gene family. Whereas several previously reported toxin gene sequences from different *B. thuringiensis* isolates with anti-Coleopteran activity were identical (EP 0149162 and 0202739), the sequences and structure of bt21 and bt22 are substantially divergent (European patent application ("EPA") 89400428.2).

While the insecticidal spectra of *B. thuringiensis* ICPs are different, the major pathway of their toxic action is believed to be common. All *B. thuringiensis* ICPs, for which the mechanism of action has been studied in any detail, interact with the midgut epithelium of sensitive species and cause lysis of the epithelial cells (Knowles and Ellar, 1986) due to the fact that the permeability characteristics of the brush border membrane and the osmotic balance over this membrane are perturbed. In the pathway of toxic action of *B. thuringiensis* ICPs, the binding of the toxin to receptor sites on the brush border membrane of these cells is an important

feature (Hofmann et al., 1988b). The toxin binding sites in the midgut can be regarded as an ICP-receptor since toxin is bound in a saturable way and with high affinity (Hofmann et al., 1988a).

Although this outline of the mode of action of *B. thuringiensis* ICPs is generally accepted, it remains a matter of discussion what the essential determinant(s) are for the differences in their insecticidal spectra. Haider et al. (1986) emphasize the importance of specific proteases in the insect midgut. Hofmann et al. (1988b) indicate that receptor binding is a prerequisite for toxic activity and describe that *Pieris brassicae* has two distinct receptor populations for two toxins. Other authors have suggested that differences in the environment of the midgut (e.g., pH of the midgut) might be crucial.

SUMMARY OF THE INVENTION

In accordance with this invention, a plant is provided having, stably integrated into its genome, at least two *B. thuringiensis* ICP genes encoding at least two non-competitively binding insecticidal *B. thuringiensis* ICPs, preferably the active toxins thereof, against a specific target insect, preferably against a Lepidoptera or Coleoptera. Such a plant is characterized by the simultaneous expression of the at least two non-competitively binding *B. thuringiensis* ICPs.

Also in accordance with this invention, at least two ICP genes, particularly two genes or parts thereof coding for two non-competitively binding anti-Lepidopteran or anti-Coleopteran *B. thuringiensis* ICPs, are cloned into a plant expression vector. Plant cells transformed with this vector are characterized by the simultaneous expression of the at least two *B. thuringiensis* ICP genes. The resulting transformed plant cell can be used to produce a transformed plant in which the plant cells: 1. contain the at least two *B. thuringiensis* ICP genes or parts thereof encoding at least two non-competitively binding anti-Lepidopteran or anti-Coleopteran *B. thuringiensis* ICPs as a stable insert into their genome; and 2. express the genes simultaneously, thereby conferring on the plant improved resistance to at least one target species of insect, so as to prevent or delay development of resistance to *B. thuringiensis* of the at least one target species of insect feeding on the transformed plant.

Further in accordance with this invention, plant expression vectors are provided which allow integration and simultaneous expression of at least two *B. thuringiensis* ICP genes in a plant cell and which comprise one or more chimeric genes, each containing in the same transcriptional unit: a promoter which functions in the plant cell to direct the synthesis of mRNA encoded by one of the ICP genes; one or more different ICP genes, each encoding a non-competitively binding *B. thuringiensis* ICP; preferably a marker gene; a 3' non-translated DNA sequence which functions in the plant cell for 3' end formation and the addition of polyadenylate nucleotides to the 3' end of the mRNA; and optionally a DNA sequence encoding a protease-sensitive protein part between any two ICP genes.

DETAILED DESCRIPTION OF THE INVENTION

Definitions

As used herein, "*B. thuringiensis* ICP" (or "ICP") should be understood as an intact protein or a part thereof which has insecticidal activity and which can be produced in nature by *B. thuringiensis*. An ICP can be a protoxin, as well as an active toxin or another insecticidal truncated part of a protoxin which need not be crystalline and which need not be a naturally occurring protein. In this regard, an ICP can be a chimaeric toxin encoded by the combination of two variable regions of two different ICP genes as disclosed in EP 0228838.

As used herein, "protoxin" should be understood as the primary translation product of a full-length gene encoding an ICP.

As used herein, "toxin", "toxic core" or "active toxin" should all be understood as a part of a protoxin which can be obtained by protease (e.g., by trypsin) cleavage and has insecticidal activity.

As used herein, "gene" should be understood as a full-length DNA sequence encoding a protein (e.g., such as is found in nature), as well as a truncated fragment thereof encoding at least the active part (i.e., toxin) of the protein encoded by the full-length DNA sequence, preferably encoding just the active part of the protein encoded by the full-length DNA sequence. A gene can be naturally occurring or synthetic.

As used herein, "truncated *B. thuringiensis* gene" should be understood as a fragment of a full-length *B. thuringiensis* gene which still encodes at least the toxic part of the *B. thuringiensis* ICP, preferentially the toxin.

As used herein, "marker gene" should be understood as a gene encoding a selectable marker (e.g., encoding antibiotic resistance) or a screenable marker (e.g., encoding a gene product which allows the quantitative analysis of transgenic plants).

Two ICPs are said to be "competitively binding ICPs" for a target insect species when one ICP competes

for all ICP receptors of the other ICP, which receptors are present in the brush border membrane of the midgut of the target insect species.

Two ICPs are said to be "non-competitively binding ICPs" when, for at least one target insect species, the first ICP has at least one receptor for which the second ICP does not compete and the second ICP has at least one receptor for which the first ICP does not compete, which receptors are present in the brush border membrane of the midgut of the target insect species.

A "receptor" should be understood as a molecule, to which a ligand (here a *B. thuringiensis* ICP, preferably a toxin) can bind with high affinity (typically a dissociation constant (K_d) between 10^{-11} and 10^{-6} M) and saturability. A determination of whether two ICPs are competitively or non-competitively binding ICPs can be made by determining whether: 1. a first ICP competes for all of the receptors of a second ICP when all the binding sites of the second ICP with an affinity in the range of about 10^{-11} to 10^{-6} M can be saturated with the first ICP in concentrations of the first ICP of about 10^{-6} M or less (e.g., down to about 10^{-11} M); and 2. the second ICP competes for all of the receptors of the first ICP when all the binding sites of the first ICP with an affinity in the range of about 10^{-11} to 10^{-6} M can be saturated with the second ICP in concentrations of the second ICP of about 10^{-6} M or less.

General Procedures

This section describes in broad terms general procedures for the evaluation and exploitation of at least two *B. thuringiensis* ICP genes for prevention of the development, in a target insect, of a resistance to the *B. thuringiensis* ICPs expressed in transgenic plants of this invention. A non-exhaustive list of consecutive steps in the general procedure follows, after which are described particular Examples that are based on this methodology and that illustrate this invention.

In accordance with this invention, specific *B. thuringiensis* ICPs can be isolated in a conventional manner from the respective strains such as are listed in Table 2 (which follows the Examples). The ICPs can be used to prepare monoclonal or polyclonal antibodies specific for these ICPs in a conventional manner (Höfte et al., 1988).

The ICP genes can each be isolated from their respective strains in a conventional manner. Preferably, the ICP genes are each identified by: digesting total DNA from their respective strains with suitable restriction enzyme(s); size fractionating the DNA fragments, so produced, into DNA fractions of 5 to 10 Kb; ligating such fractions to suitable cloning vectors (e.g., pEcoR251, deposited at the Deutsche Sammlung von Mikroorganismen und Zellkulturen ("DSMZ"), Braunschweig, Federal Republic of Germany, under accession number no. 4711 on July 13, 1988); transforming *E. coli* with the cloning vectors; and screening the clones with a suitable DNA probe. The DNA probe can be constructed from a highly conserved region which is commonly present in different *B. thuringiensis* genes which encode crystal protoxins against Coleoptera or Lepidoptera, such as on the basis of an N-terminal amino acid sequence determined by gas-phase sequencing of the purified proteins (EPA 88402115.5).

Alternatively, the desired fragments, prepared from total DNA of the respective strains, can be ligated in suitable expression vectors (e.g., a pUC vector (Yanisch-Perron et al., 1985) with the insert under the control of the lac promoter) and transformed in *E. coli*, and the clones can then be screened by conventional colony immunoprobings methods (French et al., 1986) for expression of the toxins with monoclonal or polyclonal antibodies raised against the toxins produced by the strains.

The isolated *B. thuringiensis* ICP genes can then be sequenced in a conventional manner using well-known procedures (e.g., Maxam and Gilbert, 1980).

At present, several ICP genes have been cloned from different subspecies of *B. thuringiensis* (Table 2). The nucleotide sequences from several of these *B. thuringiensis* ICP genes have been reported. whereas several sequences are identical or nearly identical and represent the same gene or slight variants of the same gene, several sequences display substantial heterogeneity and show the existence of different *B. thuringiensis* ICP gene classes. Several lines of evidence suggest that all these genes specify a family of related insecticidal proteins. Analysis of the distribution of *B. thuringiensis* ICPs in different *B. thuringiensis* strains by determining the protein composition of their crystals, by immunodetection using polyclonal antisera or monoclonals against purified crystals, or by using gene-specific probes, shows that subspecies of *B. thuringiensis* might contain up to three related *B. thuringiensis* ICP genes belonging to different classes (Kronstad et al., 1983).

To express the isolated and characterized gene in a heterologous host for purification and characterization of the recombinant protein, the preferred organism is *Escherichia coli*. A number of expression vectors for enhanced expression of heterologous genes in *E. coli* have been described (e.g., Remaut et al., 1981). Usually the gene is cloned under control of a strong regulatable promoter, such as the lambda pL or pR promoters (e.g., Botterman and Zabeau, 1987), the lac promoter (e.g., Fuller, 1982) or the tac promoter (e.g., De Boer et

al., 1983), and provided with suitable translation initiation sites (e.g., Stanssens et al., 1985 and 1987). Gene cassettes of the *B. thuringiensis* ICP genes can be generated by site-directed mutagenesis, for example according to the procedure described by Stanssens et al. (1985 and 1987). This allows cassettes to be made comprising, for example, a truncated ICP gene fragment encoding the toxic core (i.e., toxin) of an ICP or a hybrid gene encoding the toxic core and a selectable marker according to the procedures described in EPA 88402241.9.

The cells of an *E. coli* culture, which has been induced to produce a recombinant ICP, are harvested. The method used to induce the cells to produce the recombinant ICP depends on the choice of the promoter. For example, the lac promoter (Fuller, 1982) is induced by isopropyl-B-D-thiogalacto-pyranoside ("IPTG"); the pL promoter is induced by temperature shock (Bernard et al., 1979). The recombinant ICP is usually deposited in the cells as Insoluble Inclusions (Hsuing and Becker, 1988). The cells are lysed to liberate the Inclusions. The bulk of *E. coli* proteins is removed in subsequent washing steps. A semi-purified protoxin pellet is obtained, from which the protoxin can be dissolved in alkaline buffer (e.g., Na₂CO₃, pH 10). The procedure for the ICP Bt2, which is also applicable to other recombinant toxins, has been described by Höfte et al., 1986.

In accordance with this invention, the binding of various ICPs to ICP receptors on the brush border membrane of the columnar midgut epithelial cells of various insect species has been investigated. The brush border membrane is the primary target of each ICP, and membrane vesicles, preferentially derived from the brush border membrane, can be obtained according to Wolfersberger et al., 1987.

The binding to ICP receptors of one or more ICPs (e.g., ICP A, ICP B, etc.) can be characterized by the following steps (Hofmann et al., 1988b):

1. ICP A is labelled with a suitable marker (usually a radioisotope such as ¹²⁵I).
2. Brush border membranes are incubated with a small amount (preferably less than 10⁻¹⁰ M) of labelled ICP A together with different concentrations of non-labelled ICP A (preferably from less than 10⁻¹¹ to 10⁻⁵ M).
3. For all concentrations tested the amount of labelled ICP A bound to the brush border membranes is measured.
4. Mathematical analysis of these data allows one to calculate various characteristics of the ICP receptor such as the magnitude of the population of binding sites (Scatchard, 1949).
5. Competition by other toxins (e.g. ICP B) is preferably studied by incubating the same amount of labelled ICP A with brush border membranes in combination with different amounts of ICP B (preferentially from 10⁻¹¹ to 10⁻⁶ M; and subsequently, steps 3 and 4 are repeated).

By this procedure, it has been found, for example, that Bt3 toxin, Bt2 toxin and Bt73 toxin are competitively binding anti-Lepidopteran ICPs for *Manduca sexta* and *Heliothis virescens* (See example 6 which follows). Various other combinations of toxins have been found to be non-competitively binding anti-Lepidopteran or anti-Coleopteran toxins (example 6).

Although the concept of competitiveness versus non-competitiveness of ICP binding does not have any practical importance by itself, the observation of the non-competitiveness of two *B. thuringiensis* ICPs, active against the same target insect, can be put to very significant practical use. This is because a combination of two non-competitively binding *B. thuringiensis* ICPs can be used to prevent development, by a target insect, of resistance against such *B. thuringiensis* ICPs.

A selection experiment with *M. sexta*, using Bt2 toxin, Bt18 toxin, and a mixture of Bt2 and Bt18 toxins, has shown that Bt2 and Bt18 are two non-competitively binding anti-Lepidopteran toxins. After 20 generations of selection, a very pronounced reduction in ICP sensitivity was observed in the selection experiments with Bt2 or Bt18 alone (>100 times). The reduction in sensitivity in the selection experiment with a Bt2-Bt18 mixture was only marginal (3 times). This demonstrates the unexpected practical advantage of a simultaneous use of two non-competitively binding ICPs in a situation which models the high selection pressure which will exist with the use of transgenic plants transformed with ICP genes. In this regard, the two resistant strains showed a specific loss in receptor sites for either the Bt2 or Bt18 toxin. In each case, receptor sites for the toxin, which was not used for selection, were not affected or their concentration even increased. Thus, the Bt2 selected strain retained its Bt18 receptors, and the Bt18 selected strain developed an increased number of Bt2 receptors. Indeed, the Bt18 selected strain showed an increased sensitivity for Bt2 along with its increased Bt2 receptor concentration. No significant changes in receptor sites were found in the strain selected against the combined toxins. These findings are described in detail in Example 7 which follows.

A similar mechanism of resistance to Bt has been observed with respect to a strain of diamondback moth, *Plutella xylostella*. This strain had developed resistance in the field to Dipel which is a commercial formulation of the Bt HD-1 strain. Crystals of Dipel comprise a mixture of several BtICPs, similar to the Bt2, Bt3 and Bt73 proteins which are competitively-binding ICPs. As shown by both insect bioassays and competitive binding studies using Bt2 and Bt15, the Dipel-resistant diamondback moth strain is resistant to Bt2 protoxin and toxin

but maintains full sensitivity to Bt15 protoxin and toxin. This finding is relevant to other combinations of non-competitively binding anti-Lepidopteran or Coleopteran ICPs which are expected to have the same beneficial effect against their common target insects.

Hence, a combination of non-competitively binding ICPs, when directly expressed in a transgenic plant, offers the substantial advantage of reducing the chances of development of insect resistance against the ICPs expressed in the plant. There may be additional benefits because the combined spectrum of two toxins may be broader than the spectrum of a single ICP expressed in a plant (See Examples 8, 9 and 10 which follow).

If, among two competitively binding ICPs, one has a larger binding site population than the other against a given target insect, it will be most advantageous to use the one with the larger population of binding sites to control the target pest in combination with the most suitable non-competitively binding *B. thuringiensis* ICP. For example, as seen from Example 6, it is preferred to use Bt73 against *Heliothis virescens*, rather than Bt2 or Bt3, and it is preferred to use Bt3 against *Manduca sexta* rather than Bt2 or Bt73. The selected gene can then be combined with the best suitable non-competitively binding ICP.

Previously, plant transformations involved the introduction of a marker gene together with a single ICP gene, within the same plasmid, in the plant genome (e.g., Vaeck et al., 1987; Fischhoff et al., 1987). Such chimeric ICP genes usually comprised either all or part of an ICP gene, preferably a truncated ICP gene fragment encoding the toxic core, fused to a selectable marker gene, such as the *neo* gene coding for neomycin phosphotransferase. The chimeric ICP gene was placed between the T-DNA border repeats for *Agrobacterium* Ti-plasmid mediated transformation (EP 0193259).

This invention involves the combined expression of two or even more *B. thuringiensis* ICP genes in transgenic plants. The insecticidally effective *B. thuringiensis* ICP genes, encoding two non-competitively binding ICPs for a target insect species, preferably encoding the respective truncated ICP genes, are inserted in a plant cell genome, preferably in its nuclear genome, so that the inserted genes are downstream of, and under the control of, a promoter which can direct the expression of the genes in the plant cell. This is preferably accomplished by inserting, in the plant cell genome, one or more chimaeric genes, each containing in the same transcriptional unit: at least one ICP gene; preferably a marker gene; and optionally a DNA sequence encoding a protease (e.g., trypsin)-sensitive or -cleavable protein part intercalated in frame between any two ICP genes in the chimaeric gene. Each chimaeric gene also contains at least one promoter which can direct expression of its ICP gene in the plant cell.

The selection of suitable promoters for the chimaeric genes of this invention is not critical. Preferred promoters for such chimaeric genes include: the strong constitutive 35S promoter obtained from the cauliflower mosaic virus, isolates CM 1841 (Gardner et al., 1981), *cabbB-S* (Franck et al., 1980) and *cabbB-JI* (Hull and Howell, 1987); the promoter of the nopaline synthetase gene ("PNOS") of the Ti-plasmid (Herrera-Estrella, 1983); the promoter of the octopine synthase gene ("POCS" [De Greve et al., 1982]); and the wound-inducible TR1' promoter and the TR2' promoter which drive the expression of the 1' and 2' genes, respectively, of the T-DNA (Velten et al., 1984). Alternatively, a promoter can be utilized which is specific for one or more tissues or organs of the plant, whereby the inserted genes are expressed only in cells of the specific tissue(s) or organ(s). Examples of such promoters are a stem-specific promoter such as the *AdoMet*-synthetase promoter (Peleman et al., 1989), a tuber-specific promoter (Rocha-Sosa et al., 1989), and a seed-specific promoter such as the 2S promoter (Krebbers et al., 1988). The ICP genes could also be selectively expressed in the leaves of a plant (e.g., potato) by placing the genes under the control of a light-inducible promoter such as the promoter of the ribulose-1,5-bisphosphate carboxylase small subunit gene of the plant itself or of another plant such as pea as disclosed in EP 0193259. Another alternative is to use a promoter whose expression is inducible (e.g., by temperature or chemical factors).

A 3' non-translated DNA sequence, which functions in plant cells for 3' end formation and the polyadenylation of the 3' end of the mRNA sequence encoded by the at least one ICP gene in the plant cell, also forms part of each such chimeric gene. The selection of a suitable 3' non-translated DNA sequence is not critical. Examples are the 3' untranslated end of the octopine synthase gene, the nopaline synthase gene or the T-DNA gene 7 (Velten and Schell, 1985).

The selection of marker genes for the chimaeric genes of this invention also is not critical, and any conventional DNA sequence can be used which encodes a protein or polypeptide which renders plant cells, expressing the DNA sequence, readily distinguishable from plant cells not expressing the DNA sequence (EP 0344029). The marker gene can be under the control of its own promoter and have its own 3' non-translated DNA sequence as disclosed above, provided the marker gene is in the same genetic locus as the ICP gene(s) which it identifies. The marker gene can be, for example: a herbicide resistance gene such as the *sfr* or *sfrv* genes (EPA 87400141); a gene encoding a modified target enzyme for a herbicide having a lower affinity for the herbicide than the natural (non-modified) target enzyme, such as a modified 5-EPSP as a target for glyphosate (U.S. patent 4,535,060; EP 0218571) or a modified glutamine synthetase as a target for a glutamine syn-

thetase inhibitor (EP 0240972); or an antibiotic resistance gene, such as a neo gene (PCT publication WO 84/02913; EP 0193259).

Using A. tumefaciens Ti vector-mediated plant transformation methodology, all chimeric genes of this invention can be inserted into plant cell genomes after the chimaeric genes have been placed between the T-DNA border repeats of suitable disarmed Ti-plasmid vectors (Deblaere et al., 1988). This transformation can be carried out in a conventional manner, for example as described in EP 0116718, PCT publication WO 84/02913 and EPA 87400544.0. The chimeric genes can also be in non-specific plasmid vectors which can be used for direct gene transfer (e.g., as described by Pazkowski et al., 1984; De La Pena et al., 1986). Different conventional procedures can be followed to obtain a combined expression of two B.thuringiensis ICP genes in transgenic plants as summarized below.

I Chimeric gene constructs whereby two or more ICP genes and a marker gene are transferred to the plant genome as a single piece of DNA and lead to the insertion in a single locus in the genome

15 Ia The genes can be engineered in different transcriptional units each under control of a distinct promoter

To express two or more ICP genes and a marker gene as separate transcriptional units, several promoter fragments directing expression in plant cells can be used as described above. All combinations of the promoters mentioned above in the chimaeric constructs for one ICP gene are possible. Examples of such individual chimeric constructs are described for the bt2 gene in EP 0193259, for the bt13 gene in EPA 88402115.5 and for the bt18 gene in EPA 88402241.9. The ICP gene in each chimeric gene of this invention can be the intact ICP gene or preferably an insecticidally-effective part of the intact ICP gene, especially a truncated gene fragment encoding the toxic core of the ICP. The individual chimeric genes are cloned in the same plasmid vector according to standard procedures (e.g., EP 0193259).

25 Ib Two genes (e.g., either an ICP and a marker gene or two ICP genes) or more can be combined in the same transcriptional unit

To express two or more ICP genes in the same transcriptional unit, the following cases can be distinguished:

30 In a first case, hybrid genes in which the coding region of one gene is in frame fused with the coding region of another gene can be placed under the control of a single promoter. Fusions can be made between either an ICP and a marker gene or between two ICP genes. An example of an ICP gene-marker gene fusion has been described in EP 0193259 (i.e., a hybrid truncated bt2-neo gene encoding a Bt2 toxin-NPTII fusion protein).

35 Another possibility is the fusion of two ICP genes. Between each gene encoding an ICP which still is insecticidally active (i.e., a toxic part of the protoxin), a gene fragment encoding a protease (e.g., trypsin) - sensitive protein part should be included, such as a gene fragment encoding a part of the N-terminal or C-terminal amino acid sequence of one of the ICPs which is removed or cleaved upon activation by the midgut enzymes of the target insect species.

40 In a second case, the coding regions of the two respective ICP genes can be combined in dicistronic units placed under the control of a promoter. The coding regions of the two ICP genes are placed after each other with an intergenic sequence of defined length. A single messenger RNA molecule is generated, leading to the translation into two separate gene products. Based on a modified scanning model (Kozak, 1987), the concept of reinitiation of translation has been accepted provided that a termination codon in frame with the upstream ATG precedes the downstream ATG. Experimental data also demonstrated that the plant translational machinery is able to synthesize several polypeptides from a polycistronic mRNA (Angenon et al., 1989).

45 II Chimeric constructs with one or more ICP genes that are transferred to the genome of a plant already transformed with a one or more ICP genes

50 Several genes can be introduced into a plant cell during sequential transformation steps (retransformation), provided that an alternative system to select transformants is available for the second round of transformation. This retransformation leads to the combined expression of ICP genes which are introduced at multiple loci in the genome. Preferably, two different selectable marker genes are used in the two consecutive transformation steps. The first marker is used for selection of transformed cells in the first transformation, while the second marker is used for selection of transformants in the second round of transformation. Sequential transformation steps using kanamycin and hygromycin have been described, for example by Sandler

et al. (1988) and Delauney et al. (1988).

III Chimeric constructs with one or more ICP genes, that are separately transferred to the nuclear genome of separate plants in independent transformation events and are subsequently combined in a single plant genome through crosses.

The first plant should be a plant transformed with a first ICP gene or an F1 plant derived herefrom through selfing (preferably an F1 plant which is homozygous for the ICP gene). The second plant should be a plant transformed with a second ICP gene or an F1 plant derived herefrom through selfing (preferably an F1 plant which is homozygous for the second ICP gene). Selection methods can be applied to the plants obtained from this cross in order to select those plants having the two ICP genes present in their genome (e.g., Southern blotting) and expressing the two ICPs (e.g., separate ELISA detection of the immunologically different ICPs). This is a useful strategy to produce hybrid varieties from two parental lines, each transformed with a different ICP gene, as well as to produce inbred lines containing two different ICP genes through crossing of two independent transformants (or their F1 selfed offspring) from the same inbred line.

IV Chimeric constructs with one or more ICP genes separately transferred to the genome of a single plant in the same transformation experiment leading to the insertion of the respective chimeric genes at multiple loci.

Cotransformation involves the simultaneous transformation of a plant with two different expression vectors, one containing a first ICP gene, the second containing a second ICP gene. Along with each ICP gene, a different marker gene can be used, and selection can be made with the two markers simultaneously. Alternatively, a single marker can be used, and a sufficiently large number of selected plants can be screened in order to find those plants having the two ICP genes (e.g., by Southern blotting) and expressing the two proteins (e.g., by means of ELISA). Cotransformation with more than one T-DNA can be accomplished by using simultaneously two different strains of *Agrobacterium*, each with a different Ti-plasmid (Depicker et al., 1985) or with one strain of *Agrobacterium* containing two T-DNAs on separate plasmids (de Framond et al., 1986). Direct gene transfer, using a mixture of two plasmids, can also be employed to cotransform plant cells with a selectable and a non-selectable gene (Schocher et al., 1986).

The transgenic plant obtained can be used in further plant breeding schemes. The transformed plant can be selfed to obtain a plant which is homozygous for the inserted genes. If the plant is an inbred line, this homozygous plant can be used to produce seeds directly or as a parental line for a hybrid variety. The gene can also be crossed into open pollinated populations or other inbred lines of the same plant using conventional plant breeding approaches.

Of course other plant transformation methods can be used and are within the scope of the invention as long as they result in a plant which expresses two or more non-competitively binding ICPs. In this regard, this invention is not limited to the use of *Agrobacterium* Ti-plasmids for transforming plant cells with genes encoding non-competitively binding ICPs. Other known methods for plant cell transformations, such as electroporation or by the use of a vector system based on plant viruses or pollen, can be used for transforming monocotyledonous and dicotyledonous plants in order to obtain plants which express two non-competitively binding ICPs. Furthermore, DNA sequences encoding two non-competitively binding ICPs other than those disclosed herein can be used for transforming plants. Also, each of the ICP genes, described herein, can be encoded by equivalent DNA sequences, taking into consideration the degeneracy of the genetic code. Also, equivalent ICPs with only a few amino acids changed, such as would be obtained through mutations in the ICP gene, can also be used, provided they encode a protein with essentially the same characteristics (e.g., insecticidal activity and receptor binding).

The following Examples illustrate the invention. Those skilled in the art will, however, recognize that other combinations of two or more non-competitively binding *B. thuringiensis* ICP genes can be used to transform plants in accordance with this invention in order to prevent the development, in a target insect, of resistance to *B. thuringiensis* ICPs expressed in the transformed plants. Unless otherwise indicated, all procedures for making and manipulating DNA were carried out by the standardized procedures described in Maniatis et al, *Molecular Cloning - A Laboratory Manual*, Cold Spring Harbor Laboratory (1982).

EXAMPLE 1: Collection of genes

The collection of anti-Lepidopteran and anti-Coleopteran Bt genes encoding ICPs, which are the subject of the Examples, is described in Table 2 (following the Examples). References for the respective genes are

indicated in Table 2. The origin, the isolation and characterization of the Bt genes, which have not been published, are described below. Bt strains, such as strains HD-1, HD-68, HD-110, and HD-73, are publicly available from the Agricultural Research Culture Collection, Northern Regional Research Laboratory, U.S. Dept. of Agriculture, Peoria, Illinois 61604, U.S.A.

- 5 **bt3 gene:** From B. thuringiensis var. kurstaki HD-1, the ICP was cloned. Characterization of this gene revealed an open reading frame of 3528 bp which encodes a protoxin of 133 kDa. This gene was identical to the one described by Schnepf et al. (1985).
- bt73 gene:** From B. thuringiensis var HD-73. The ICP gene was cloned as described by Adang et al. (1985).
- 10 **bt4 gene:** A genomic library was prepared from total DNA of strain B. thuringiensis aizawai HD-68. Using the 1.1 kb internal HindIII fragment of the bt2 gene as a probe, a gene designated bt4 was isolated. Characterization of this gene revealed an open reading frame of 3495 bp which encodes a protoxin of 132 kDa and a trypsin activated toxin fragment of 60 kDa. This (insect controlling protein) gene differs from
- 15 previously identified genes and was also found in several other strains of subspecies aizawai and entomocidus including HD-110. Fig. 13 shows the nucleotide sequence and deduced amino acid sequence of the open reading frame ("ORF") of the bt4 gene extending from nucleotide 264 to nucleotide 3761.
- bt14 and bt15 genes:** A genomic library was prepared from total DNA of strain B. thuringiensis var. entomocidus HD-110 by partial Dau3A digest of the total DNA and cloning in the vector pEcoR251 (deposited at DSM under accession number 4711). Using monoclonal antibodies (Höfte et al., 1988), at least three structurally distinct ICPs were identified in crystals of B. thuringiensis entomocidus HD-110. These monoclonal antibodies were used to clone the three different ICP genes from this B. thuringiensis strain. One of these genes is the bt4 gene as described above.
- 20 The second gene was called "bt15". Fig. 14 shows the nucleotide sequence and deduced amino acid sequence of the ORF of the bt15 gene, isolated from HD-110, extending from nucleotide 234 to nucleotide 3803. The Shine and Dalgarno sequence, preceding the initiation codon is underlined. This gene has an open reading frame of 3567 bp which encodes a protoxin of 135 kDa and a 63 kDa toxin fragment. A similar gene has been
- 30 described by Honnee et al. 1988, isolated from B. thuringiensis entomocidus 60.5. The bt15 gene differs from the published sequence at three positions: an Ala codon (GCA) is present instead of an Arg codon (CGA) at position 925 and a consecution of a Thr-His codon (ACGCAT) is present instead of a Thr-Asp codon (ACCGAT) at position 1400. (The numbers of the positions are according to Honnee et al., 1988). Another similar gene has been described in EP 0295156, isolated from B. thuringiensis aizawai 7-29 and entomocidus 6-01. The
- 35 bt15 gene is different from this published nucleotide sequence at three different places : 1) a Glu codon (GAA) instead of an Ala codon (GCA) at position 700; 2) the sequence TGG, CCA, GCG, CCA instead of TGC, CAG, CGC, CAC, CAT at position 1456 and 3) an Arg codon (CGT) instead of an Ala codon (GCG) at position 2654. (The numbers of the positions are according to EP 0295156).
- The third gene isolated was called "bt14". It has an open reading frame of 3621 bp which encodes a 137 kDa protoxin and a 66 kDa activated toxin fragment. A similar gene has been cloned from B. thuringiensis HD-2 (Brizzard and Whiteley, 1988). The bt14 gene differs from the published nucleotide sequence by two nucleotide substitutions: a T instead of a C at position 126, and a C instead of a T at position 448 (the numbers of the positions are according to Brizzard and Whiteley, 1988). In the first case, the Ile codon (ATT or ATC) is conserved whereas in the second case the Tyr codon (TAT) is converted to a His codon (CAC).
- 40 The bt2 gene was cloned as described in EP 0193259.
- 45 **bt2 gene:** The bt2 gene was cloned as described in EP 0193259.
- bt18 gene:** Cloning of the bt18 gene was performed as described in EPA 88402241.9.
- bt13 gene:** The bt13 gene was cloned as described in EPA 88402115.5.
- bt21 and bt22 genes:** These genes, encoding Coleopteran-active ICPs, were cloned as described in EPA 89400428.2.

EXAMPLE 2 : Construction of gene cassettes and expression of Bt genes in E.coli

- 1) bt2, bt18: the construction of bt2 and bt18 gene cassettes has been previously described in EPA 86300291.1 and 88402241.9, respectively. Basically, they comprise a truncated gene encoding the toxic core and a hybrid gene comprising the truncated gene fused in frame to the N-terminus of the neo gene. The gene cassettes are used to transform E. coli to express the Bt2 and Bt18 ICP toxins.
- 2) bt14, bt15: as described in EPA 88402241.9, gene cassettes for the bt14 and bt15 genes were constructed in order to express the genes in E.coli and in plants.

First, a NcoI site was introduced at the N-terminus of the genes by site-directed mutagenesis.

In the case of the bt15 gene, the conversion of the TT nucleotides, immediately in front of the ATG codon, into CC yielded a NcoI site overlapping with the ATG initiation codon. This site was introduced using the pMa/c vectors for site-directed mutagenesis (Stanssens et al., 1987) and a 28-mer oligonucleotide with the following sequence:

5' -CGGAGGTATTCCATGGAGGAAAATAATC-3'.

This yielded the plasmid pVE29 carrying the N-terminal fragment of the bt15 gene with a NcoI site at the ATG initiation codon.

According to Brizzard and Whiteley (1988), the initiation codon of the bt14 gene is a TTG codon. Thus, a NcoI site was created in a like manner at this codon for site directed mutagenesis using a 34-mer oligonucleotide with the following sequence :

5' -CCTATTTGAAGCCATGGTAACTCCTCCTTTTATG-3'.

In this case the sequence of the initiation codon was converted from ATATTGA to ACCATGG. This yielded the plasmid pHW44 carrying the N-terminal fragment of the bt14 gene with a NcoI site at the initiation codon.

In a second step, the genes were reconstructed by ligating the N-terminal gene fragments with a suitable C-terminal gene fragment, yielding a bt15 gene and bt14 gene with a NcoI site at the ATG initiation codon.

To express the bt14 and bt15 genes encoding the protoxin in *E. coli*, the following constructs were made: POH50 containing the bt15 gene under the control of the lac promoter; and pHW67 containing the bt14 gene under the control of the tac promoter. Induction of a culture of the *E. coli* strain WK6 carrying the respective plasmids with IPTG yielded an overproduced protein (Fuller, 1982).

The active toxic fragments of the Bt15 and Bt14 protoxins comprise 63 and 60 kDa trypsin digest products respectively. Instead of expressing the whole bt15 or bt14 gene, it is also possible to express a toxin-encoding gene fragment or derivative thereof in plants. To this end, truncated bt14 and bt15 gene fragments were constructed. In order to be able to select transgenic plants producing the ICP gene products, hybrid genes of the truncated gene fragments were also made with the neo gene encoding a selectable marker as described in EP 0193259.

By comparison of the nucleotide sequence of the bt4, bt14 and bt15 genes, respectively, with the bt2 and bt18 genes, respectively, the BclI site could be identified as a suitable site localized downstream of the coding sequence encoding the toxin gene fragment. To construct a truncated gene fragment and a hybrid gene of the truncated gene fragment with the neo gene, the filled BclI site was ligated to the filled EcoRI site of pLKM91 (Höfte et al., 1986) and the filled HindIII site of pLK94 respectively (Botterman and Zabeau, 1987). pLKM91 carries a 5' truncated neo gene fragment which codes for an enzymatically active C-terminal gene fragment of the neo gene, and pLK94 contains translation stop codons in three reading frames. This yielded the following plasmids which are then used to transform *E. coli* to express the ICP genes: pHW71 carrying a truncated bt14-neo hybrid gene; pHW72 carrying a truncated bt14 gene; pVE34 carrying a truncated bt15-neo hybrid gene; and pVE35 carrying a truncated bt15 gene.

In a similar way as described for the bt14 and bt15 genes, gene cassettes are constructed for the bt3 and bt4 genes which are then expressed in *E.coli*.

EXAMPLE 3: Purification of recombinant ICPs

The ICPs expressed in *E. coli* in Example 2 are purified by the method (described for recombinant Bt2 protoxin) by Höfte et al. (1986).

EXAMPLE 4: Purification of toxins

Solubilized protoxins of Bt2, Bt3, Bt73, Bt4, Bt14, Bt15, Bt18, Bt13, Bt21 and Bt22 (in Na₂CO₃ 50mM, DTT 10 mM pH=10) are dialyzed against 0.5 % (NH₄)₂CO₃ at pH 8 and treated with trypsin (trypsin/protoxin=1/20 w/w) for 2h at 37°C. The activated toxin is chromatographically purified (Mono-Q column on FPLC) as described by Hofmann et al.(1988b).

EXAMPLE 5: Determination of the insecticidal spectrum

The ICP protoxins and toxins of Examples 3 and 4 are evaluated for their insecticidal activity. Each protoxin

is dissolved in alkaline buffer containing a reducing agent (Na_2CO_3 50 mM, DTT 10 mM pH=10), and each toxin is used as soluble protein directly from FPLC. Protein concentrations are determined. Subsequently, dilutions of the resulting protoxin or toxin solution are prepared in PBS buffer pH=7.4 containing 0.15 M NaCl and 0.1 % bovine serum albumin ("BSA").

5 The artificial medium for insect culture, described by Bell and Joachim (1976) for *Manduca sexta*, is poured in appropriate receptacles and allowed to solidify. Subsequently a quantity of the (pro) toxin dilutions is applied on this medium, and the water is allowed to evaporate under a laminar flow. This results in a medium with a certain quantity (in the range of 0.1 to 10000 ng/cm²) of toxin coated on its surface. For example, for the Bt2 toxin, typical dilutions for a toxicity test on *Manduca sexta* are 1, 5, 25, 125 and 625 ng/cm². First instar larvae
10 of *Manduca sexta* are then applied on the coated medium, and growth and mortality are assessed after 6 days. Mortality increases with dosage. Dose response data is analysed in probit analysis (Finney, 1962), and the data are best summarized by an LD₅₀ value which is the amount of toxin which kills 50 % of the insects. The LD₅₀ for Bt2 toxin against *Manduca sexta* is around 20 ng/cm².

Similar assays are carried out for other insect species using a suitable diet or by applying the ICPs on
15 leaves for insects, for which no artificial diet is used.

EXAMPLE 6: Binding studies

Toxins

20 All protoxins and their toxic fragments were purified according to the methods described for the Bt2 protoxin and toxin in Höfte et al. (1986) and EP 0193259. The activated and purified toxins are further referred to as the Bt2, Bt3, Bt73, Bt4, Bt14, Bt15, Bt18, Bt13, Bt21 and Bt22 toxins.

By way of example for the Bt73 toxin, it has been shown that *B. thuringiensis* var. *kurstaki* HD73 produces
25 a protein of 133 kDa encoded by a 6.6 kb type gene. A culture of this strain was grown as described by Mahillon and Delcour (1984). The autolysed culture was spun down (20 minutes at 4500 rpm in a HB4 rotor) and washed with a buffer containing 20 mM Tris, 100 mM NaCl and 0.05 % Triton X-100, pH 8. The final pellet was resuspended in this buffer (4 ml buffer for 100 ml culture). This solution was then layered onto a linear Urografin gradient (60-70%) which was centrifuged in a SW 28 rotor for 90 minutes at 18000 rpm. Crystals were collected
30 and stored at -20°C until further use. Activation was performed according to Höfte et al. (1986). The purified toxin is further referred to as the Bt73 toxin.

Iodination of ICPs

35 Iodination of Bt2, Bt3, and Bt73 toxins was performed using the Chloramin-T method (Hunter and Greenwood, 1962). 1 mCi ¹²⁵I-Nal and 20 to 37.5 ug Chloramin-T in NaCl/P_i were added to 50 ug of purified toxin. After gentle shaking for 60 seconds, the reaction was stopped by adding 53 ug of potassium metabisulfite in H₂O. The whole mixture was loaded on a PD 10 Sephadex G-25M gelfiltration column to remove free iodine. A subsequent run on a Biogel P-60 column was carried out in order to increase the purity.

40 Alternatively, toxins were labeled using the Iodogen method. Iodogen (Pierce) was dissolved in chloroform at 0.1 mg/ml. 100 ul of this solution was pipetted into a disposable glass vessel and dried under a stream of nitrogen gas. The vessel was rinsed with Tris buffer (20 mM Tris, pH 8.65 with 0.15 M NaCl). 50 ug of toxin (in Tris buffer) was incubated with 1 mCi of ¹²⁵I-Nal in the tube for 10 minutes. The reaction was then stopped by the addition of 1 M NaI (one fourth of the sample volume). The sample was immediately loaded onto a
45 PD10 Sephadex G-25M column and later on a Biogel P-60 column to remove free iodine and possible degradation products.

Other toxins were iodinated using one of the above mentioned procedures.

Determination of specific activity of iodinated toxin

50 Specific activity of iodinated Bt2, Bt3, and Bt73 toxin samples was determined using a "sandwich" ELISA technique according to Voller, Bidwell and Barlett (1976). Primary antibody was a polyclonal antiserum raised against Bt2 toxin, and the secondary antibody was a monoclonal antibody 4D6.

The conjugate used was alkaline phosphatase coupled to anti-mouse IgG. The reaction intensity of a standard dilution series of unlabeled toxin and dilutions of the iodinated toxin sample (in NaCl/P_i - 0.1 % BSA) was
55 measured. Linear regression calculations yielded the protein content of the radioactive toxin sample. The samples with the highest specific activities were used in the binding assays. Specific activities were 59400, 33000 and 19800 Ci/mole (on reference date) for Bt73 toxin (labeled according to Iodogen procedure), Bt2 toxin (Chlor-

amin-T method) and Bt3 toxin (Iodogen method) respectively.

Specific activities of other toxins were determined using a similar approach. Specific monoclonal and polyclonal antibodies for each of these toxins were raised and applied in ELISA.

5 Preparation of brush border membrane vesicles

Brush border membrane vesicles ("BBMV") from *Manduca sexta*, *Heliothis virescens*, *Plutella xylostella*, *Phthorimaea operculella*, *Spodoptera exigua*, *Spodoptera littoralis*, *Plodia interpunctella*, *Mamestra brassicae*, *Pieris brassicae* and *Leptinotarsa decemlineata* were prepared according to the method of Wolfersberger et al. (1987). This is a differential centrifugation method that makes use of the higher density of negative electrostatic charges on luminal than on basolateral membranes to separate these fractions.

Binding assay

15 Duplicate samples of ^{125}I -labeled toxin, either alone or in combination with varying amounts of unlabeled toxin, were incubated at the appropriate temperature with brush border membrane vesicles in a total volume of 100 μl of Tris buffer (Tris 10 mM, 150 mM NaCl, pH 7.4). All buffers contained 0.1 % BSA. The incubation temperature was 20 $^{\circ}\text{C}$. Ultrafiltration through Whatman GF/F glass fiber filters was used to separate bound from free toxin. Each filter was rapidly washed with 5 ml of ice-cold buffer (NaCl/P_r 0.1 % BSA). The radioactivity of the filter was measured in a gammacounter (1275 Minigamma, LKB). Binding data were analyzed using the LIGAND computer program. This program calculates the bound concentration of ligand as a function of the total concentration of ligand, given the affinity (K_a or its inverse $K_d = 1/K_a$, the dissociation constant) and the total concentration of receptors or binding site concentration (R_t).

25 Determination of protein concentration

Protein concentrations of purified Bt2, Bt3, Bt73 and Bt15 toxins were calculated from the OD at 280 nm (measured with a Uvikon 810 P, Kontron Instruments spectrophotometer). The protein content of solutions of other toxins and of brush border membrane vesicles (BBMV) as measured according to Bradford (1976).

30 Binding of Bt2, Bt3 and Bt73 toxins to BBMV of *Manduca sexta* and *Heliothis virescens*: an example of 3 competitively binding Lepidopteran ICPs.

Bt2, Bt3 and Bt73 toxins are toxic to both *Manduca sexta* and *Heliothis virescens*: LC50 values for *Manduca sexta* are respectively 17.70, 20.20 and 9.00 ng/cm²; for *Heliothis virescens* the LC50's are 7.16, 90.00 and 1.60 ng/cm².

Labelled toxin, either Bt3 (0.8 nM) or Bt2 (1.05 nM) or Bt73 (1.05 nM), was incubated with BBMV in a volume of 0.1 ml. BBMV protein concentrations were 100 $\mu\text{g}/\text{ml}$ for *M. sexta* and for Bt2-*H. virescens*, for Bt3-*H. virescens* 150 and for Bt73-*H. virescens* 50 $\mu\text{g}/\text{ml}$. The labelled toxin was combined with varying amounts of an unlabeled toxin (competitor). After a 30 min. incubation, bound and free toxins were separated through filtration.

Figs. 1-3 show the percentages binding of respectively labelled Bt2, Bt3 and Bt73 toxins as a function of the concentration of competitor for *Manduca sexta*. Figs. 4-6 show these data for *Heliothis virescens*. The amount bound in the absence of competitor is always taken as 100 % binding. Figs. 1-6 show the binding of ^{125}I -labeled toxins to *M. sexta* (in Figs. 1, 2 and 3) and *H. virescens* (in Figs. 4, 5 and 6) brush border membrane vesicles. Vesicles were incubated with labeled toxin [in Figs. 1 and 4: ^{125}I -Bt2-toxin (1.05nM); in Figs. 2 and 5: ^{125}I -Bt3-toxin (0.8nM); in Figs. 3 and 6: ^{125}I -Bt73-toxin (1.05nM)] in the presence of increasing concentrations of Bt2 toxin (*), Bt3 toxin (●) or Bt73 toxin (▲). Binding is expressed as percentage of the amount bound upon incubation with labeled toxin alone. On *M. sexta* vesicles, these amounts were 1820, 601 and 2383 cpm, and on *H. virescens* vesicles 1775, 472 and 6608 cpm for ^{125}I -Bt2-, Bt3- and Bt73-toxin, respectively. Non-specific binding was not subtracted. Data were analyzed with the LIGAND computer program. Each point is the mean of a duplicate sample.

Figure 1: shows the binding of ^{125}I Bt2 toxin to *M. sexta* BBMV
 Figure 2: shows the binding of ^{125}I Bt3 toxin to *M. sexta* BBMV
 Figure 3: shows the binding of ^{125}I Bt73 toxin to *M. sexta* BBMV
 Figure 4: shows the binding of ^{125}I Bt2 toxin to *H. virescens* BBMV
 Figure 5: shows the binding of ^{125}I Bt3 toxin to *H. virescens* BBMV
 Figure 6: shows the binding of ^{125}I Bt73 toxin to *H. virescens* BBMV

The conclusions from Figures 1-6 are that Bt2 and Bt3, Bt3 and Bt73, and Bt2 and Bt73 are competitively-binding ICP's both for Manduca sexta and for Heliothis virescens. Indeed Bt3 competes for the entire population of receptor sites of Bt2 in Manduca sexta (Fig.1): the % labelled Bt2 bound in the presence of 100 nM Bt3 is equal to the % Bt2 bound with 100 nM of Bt2 itself. The opposite is not true: in the presence of 100 nM Bt2 the % of labelled Bt3 is not reduced to the same level as with 100 nM of Bt3 (Fig.2).

A similar reasoning is followed to observe competitiveness of other toxin combinations : Bt3 competes for the entire population of receptor sites of Bt73 (Fig. 3) in M. sexta; the opposite is not true (Fig. 2); Bt2 and Bt73 compete for the entire population of each other's binding sites in M. sexta (Figs. 1 and 3).

In Heliothis virescens : Bt2 competes for the entire population of receptor sites of Bt3 (Fig. 5); Bt73 competes for the entire population of receptor sites of Bt3 (Fig. 5); Bt73 competes for the entire population of receptor sites of Bt2 (Fig. 4); but the opposite statements are not true (Figs. 4, 5 and 6).

The same data can be used in mathematical analysis (e.g., Scatchard analysis according to Scatchard, 1949; analysis with the LIGAND computer program according to Munson and Rodbard, 1980) to calculate the dissociation constant (Kd) of the toxin-receptor complex and the concentration of binding sites (Rt); the results of these calculations using the LIGAND computer program were the following:

Bt2- <u>M. sexta</u> :	Kd=0.4 nM	Rt=3.4 pmol/mg vesicle protein
Bt3- <u>M. sexta</u> :	Kd=1.5 nM	Rt=9.8 pmol/mg vesicle protein
Bt73- <u>M. sexta</u> :	Kd=0.6 nM	Rt=4.0 pmol/mg vesicle protein
Bt2- <u>H. virescens</u> :	Kd=0.6 nM	Rt=9.7 pmol/mg vesicle protein
Bt3- <u>H. virescens</u> :	Kd=1.2 nM	Rt=3.7 pmol/mg vesicle protein
Bt73- <u>H. virescens</u> :	Kd=0.8 nM	Rt=19.5 pmol/mg vesicle protein

These data demonstrate the high affinity receptor binding of the toxins (Kds in the range of 10^{-10} to 10^{-9} M).

Binding of Bt2 and Bt14 toxins to BBMV of P. brassicae Plutella xylostella and Phthorimaea operculella: an example two non-competitively binding Lepidopteran ICPs

Bt2 and Bt14 toxins are toxic to P. brassicae (p.b.), P. xylostella (p.x.) and P. operculella (p.o.) as seen from the table below.

LC ₅₀ of Toxins		
	Bt2	Bt14
P.b.	1.3	2.0
P.x.	6.7	5.4
P.o.	4.20	0.8-4.0

LC₅₀ values of solubilized purified Bt2 and Bt14 toxins for P.x. are expressed as ng protein spotted per cm² of artificial diet. LC₅₀ values for P.b. are expressed as ug² toxin per ml solution into which leaf discs, fed to first instar Pb larvae, were dipped. For P.o., LC₅₀ values are expressed in ug/ml into which potato chips were dipped prior to feeding.

Labelled Bt2 toxin (1.05 nM) or Bt14 toxin (1.4 nM) was incubated with BBMV from *P. brassicae* (100 ug protein/ml) in a volume of 0.1 ml in combination with varying amounts of unlabelled Bt2 or Bt14. After a 30 min. incubation period at 22°C, the bound and free toxins were separated.

Figures 7 and 8 show the binding of ¹²⁵I-labeled toxins to *P. brassicae* brush border membrane vesicles. Vesicles were incubated with labeled toxin [in Fig. 7: ¹²⁵I-Bt2-toxin (1.05nM) in Fig. 8: ¹²⁵I-Bt14-toxin (1.4nM)] in the presence of increasing concentrations of Bt2 toxin (○) or Bt14 toxin (●). Binding is expressed as percentage of the amount bound upon incubation with labeled toxin alone. Non-specific binding was not subtracted. Data were analyzed with the LIGAND computer program. Each point is the mean of a duplicate sample. Figure 7 shows the binding of labelled Bt2 toxin to *P. brassicae* BBMV, and Figure 8 shows the binding of labelled Bt14 toxin to *P. brassicae* BBMV.

The competition data demonstrate the presence of high affinity binding sites both for Bt2 and Bt14, as well as the almost complete absence of competition of Bt14 for the Bt2 binding sites and of Bt14 for the Bt2 binding sites. This demonstrates that Bt2 and Bt14 are non-competitively binding toxins. Hence they are useful to prevent the development of *Pieris brassicae* resistance against *B. thuringiensis* ICP's expressed in *Brassica* sp.

Calculated Kd and Rt values were from these experiments were:

Bt2: Kd=2.8 nM, Rt=12.9 pmol/mg vesicle protein

Bt14: Kd=8.4 nM, Rt=21.4 pmol/mg vesicle protein.

20 Binding of Bt2 and Bt15 toxins to BBMV of *M. sexta*, *M. brassicae*, *P. xylostella* and *P. interpunctella* : an example of two non-competitively binding Lepidopteran ICPs

Bt2 and Bt15 toxins are both toxic to *M. sexta* (LC50's of 20 and 111 ng/cm², respectively). They also show activity against *M. brassicae*, *P. xylostella* and *P. interpunctella*.

Labelled Bt2 (1.05 nM) or Bt15 (0.7 nM) was incubated with BBMV from *M. sexta* (100 ug protein/ ml) in a volume of 0.1 ml in combination with varying amounts of unlabelled Bt2 or Bt15. After a 30 min. incubation period at 22°C, the bound and free toxins were separated.

Figs. 9-10 show the binding of ¹²⁵I-labeled toxins to *M. sexta* brush border membrane vesicles. Vesicles were incubated with labeled toxin [in Fig. 9: ¹²⁵I-Bt2-toxin (1.05nM); in Fig. 10: ¹²⁵I-Bt15-toxin (0.7nM)] in the presence of increasing concentrations of Bt2-toxin (○) or Bt15-toxin (●). Binding is expressed as percentage of the amount bound upon incubation with labeled toxin alone. Non-specific binding was not subtracted. Data were analyzed with the LIGAND computer program. Each point is the mean of a duplicate sample. Figure 9 shows the data for binding of labelled Bt2, and Figure 10 shows the binding of labelled Bt15.

The competition data demonstrate the presence of high affinity binding sites for both Bt2 and Bt15, as well as the complete absence of competition of Bt15 for the Bt2 binding sites and of Bt2 for the Bt15 binding sites. This demonstrates that Bt2 and Bt15 are non-competitively binding toxins. Hence the combination of Bt2 and Bt15 is useful to prevent the development of resistance of *M. sexta* against *B. thuringiensis* ICP's expressed in tobacco or other crops in which *Manduca* sp. are a pest. Calculated Kd and Rt values are:

Bt2: Kd=0.4 nM, Rt=3.4 pmol/mg vesicle protein Bt15: Kd = 0.3 nM Kd2=2.9 nM, Rt1= 5.9 and Rt2=6.7 pmol/mg vesicle protein (2 distinct high affinity receptor sites are present).

Similar studies were performed for *M. brassicae*, *S. littoralis* and *P. interpunctella*. Although LD50, Kd and Rt values differed substantially, the essential observation that Bt2 and Bt15 are both toxic and are non-competitively binding toxins was confirmed in these three insect species. Thus, it is also a useful toxin combination to prevent resistance of *M. brassicae* to ICP's or to prevent resistance of *Spodoptera* species against ICP's expressed in any of the crop plants in which *Spodoptera* species are a pest.

Binding of Bt2 and Bt4 toxins to BBMV of *M. sexta*: an example of two non-competitively binding Lepidopteran ICPs

Both Bt2 and Bt4 toxins are toxic to *Manduca sexta*. LD50 values are 20 and 5.4. ng/cm², respectively. No mutual competition of Bt2 for binding of labelled Bt4 and of Bt4 for binding of labelled Bt2 was observed, demonstrating that Bt2 and Bt4 are non-competitively binding toxins.

55 Binding of Bt15 and Bt18 toxins to BBMV of *S. littoralis*: an example of two non-competitively binding Lepidopteran ICPs

Both Bt15 and Bt18 toxins are toxic to *S. littoralis*. LD 50 values are 93 and 88 ng toxin/cm², respectively. Labelled Bt15 (0.7 nM) or Bt18 (0.9 nM) was incubated with 100 ug of vesicle protein from *S. littoralis* in com-

bination with varying amounts of unlabelled Bt15 or Bt18 toxin. After a 45 min. incubation period, bound and free toxins were separated. Binding data demonstrate high affinity binding for both Bt15 and Bt18 to S. littoralis BBMV. As seen from Figures 11 and 12, the entire population of receptor sites of Bt15 was not saturable with Bt18, nor was the entire population of receptor sites of Bt18 saturable with Bt15.

5

Binding of Bt13 and Bt22 toxins to BBMV of *L. decemlineata* : an example of two non-competitively binding Coleopteran ICPs.

10

Both Bt13 and Bt22 toxins are toxic to L. decemlineata. LD 50 values are 0.8 and 1.1 ug toxin/ml respectively. Labelled Bt13 (1 nM) or Bt22 (0.7 nM) was incubated with 100 ug of vesicle protein/ml from S. littoralis BBMV. In combination with varying amounts of unlabelled Bt13 or Bt22 toxin. After a 45 min. incubation period, bound and free toxins were separated. Binding data demonstrate high affinity binding for both Bt13 and Bt22 to S. littoralis BBMV. The entire population of receptor sites of Bt13 was not saturable with Bt22. Nor was the entire population of receptor sites of Bt22 saturable with Bt13.

15

Binding of Bt2 and Bt18 toxins to BBMV of *M. sexta*: an example of two non-competitively binding Lepidopteran ICPs.

20

Both Bt2 and Bt18 toxins are toxic to M. sexta, and LD 50 values are 20 to 73 ng toxin/cm² respectively. Labelled Bt2 (1.05nM) or Bt18 (0.7nM) was incubated with 100 ug/ml of vesicle protein from M. sexta in combination with varying amounts of unlabelled Bt2 or Bt18 toxin. After a 45 min. incubation period, bound and free toxins were separated. Binding data (Figs. 11-12) demonstrate high affinity binding for both Bt2 and Bt18 to M. sexta BBMV. The entire population of receptor sites of Bt2 was not saturable with Bt18. Nor was the entire population of receptor sites of Bt18 saturable with Bt2. Calculated Kd and Rt values are:

25

Bt2: Kd= 0.4 nM, Rt= 3.4 pmol/mg vesicle protein. Bt18: Kd1= 0.04 nM, Rt1= 2.2 pmoles/mg vesicle protein and Kd2= 168nM Rt2= 194 pmoles/mg vesicle protein (2 distinct receptor sites for Bt18 are present).

A list of non-competitively binding anti-Lepidopteran ICP combinations and anti-Coleopteran ICP combinations is given below, together with their common target insect species in which non-competitiveness has been demonstrated:

30

Bt2-Bt15 (Manduca sexta, Plutella xylostella, Pieris brassicae, Mamestra brassicae, Plodia interpunctella)

Bt2-Bt18 (Manduca sexta, Spodoptera littoralis)

Bt2-Bt14 (Pieris brassicae, Plutella xylostella, Phthorimaea operculella)

Bt2-Bt4 (Manduca sexta)

35

Bt15-Bt18 (Manduca sexta, Spodoptera littoralis)

Bt14-Bt15 (Pieris brassicae)

Bt15-Bt4 (Manduca sexta, Spodoptera exigua)

Bt18-Bt4 (Manduca sexta, Spodoptera littoralis)

Bt18-Bt14 (Pieris brassicae)

40

Bt18-Bt4 (Manduca sexta)

Bt13-Bt21 (Leptinotarsa decemlineata)

Bt13-Bt22 (Leptinotarsa decemlineata)

Bt21-Bt22 (Leptinotarsa decemlineata)

45

Of course, this list of specific non-competitively binding ICP combinations for specific target insect pests is not exhaustive, and it is believed that other such ICP combinations, including combinations for yet-to-be discovered ICPs, will be found using a similar approach for any target insect species. Likewise, the foregoing list of target insect pests also is not exhaustive, and it is believed that other target insects pests (as well as the plants that are to be transformed to prevent their attack by such pests), against which the specific combinations of ICPs can be used (e.g., the combination of the Bt2 and Bt14 ICPs in Brassica to prevent resistance of Pieris brassicae against the ICPs expressed in the plant), will be found using a similar approach.

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EXAMPLE 7: Selection for resistance of *Manduca sexta* (tobacco hornworm)

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A selection experiment involves exposing a large number of larvae to a concentration of a toxin in a diet killing (e.g., 50-90 %) of the larvae. The surviving larvae are again exposed to toxin concentrations killing a similar proportion of the larvae, and this process is continued for several generations. The sensitivity of the larvae to the toxin is investigated after each four generations of selection.

Selections for 20 generations of M. sexta were performed with Bt2 toxin alone, with Bt18 toxin alone and

with a 1/4 (by weight) Bt2/Bt18 mixture. LC50 values of the reference strain for Bt2, Bt18 and the 1/4 Bt2/Bt18 mixture respectively were the following : 20 ng/cm², 73 ng/cm² and 62 ng/cm² of diet.

Selection was initiated at concentrations killing around 75 % of the larvae. After 4 generations of selection, survival increased in both the Bt2 and the Bt18 selection to around 70 %, no such increase was observed in the selection with the combination of Bt2 and Bt18. Dosages were again increased to calculated LC75 values. This was repeated every 4 generations. The selection process was thus continued to the 20th generation. Final results were the following (LC50 of the 20th generation):

- Bt2 selection: LC50 was 6400 ug/g (320 times decreased sensitivity)
- Bt18 selection: LC50 was 15100 ug/g (207 times decreased sensitivity)
- Bt2/Bt18 selection: LC50 was 181 ug/g (3 times decreased sensitivity).

Thus the decrease in sensitivity was about 100 times slower in the combined selection experiment.

Receptor binding in the three selected *M. sexta* strains was investigated with Bt2 and Bt18 and compared to those of the reference *M. sexta* strain (non-selected strain). Binding characteristics of the reference strain for the Bt2 and Bt18 toxins were:

Bt2: Kd = 0.4 nM, Rt=3.4 pmol/mg vesicle protein

Bt18: Kd1=0.04 nM, Rt1=2.2 pmoles/mg vesicle protein and Kd2=168nM, Rt2=194 pmoles/mg vesicle protein (2 distinct receptor sites for Bt18 are present).

Figures 11 and 12 show the binding of ¹²⁵I-labeled toxins to *M. sexta* brush border membrane vesicle. Vesicles were incubated with labeled toxin [in Fig. 11: ¹²⁵I-Bt2-toxin (1.05nM); in Fig. 12: ¹²⁵I-Bt18-toxin (0.7nM)] in the presence of increasing concentrations of Bt2-toxin (○) or Bt18-toxin (●). Binding is expressed as percentage of the amount bound upon incubation with labeled toxin alone. Non-specific binding was not subtracted. Data were analyzed with the LIGAND computer program. Each point is the mean of a duplicate sample.

The Bt2 selected strain showed no detectable high affinity binding of Bt2 whereas its Bt18 binding characteristics remained close to the reference strain. (Bt18: Kd1=0.03 nM, Rt1=2.8 pmoles/mg vesicle protein and Kd2=199nM, Rt2=109 pmoles/mg vesicle protein; 2 distinct receptor sites for Bt18 are still present).

The Bt18 selected strain lost the high affinity receptor site for Bt18. The lower affinity site for Bt18 was still present in lower concentration than in the reference strain (Kd=189 nM, Rt=43 nM). Bt2 binding site concentration increased markedly compared to the reference strain (Kd=0.4 nM, Rt=20.8 pmoles/mg vesicle protein). This strain had a Bt2 sensitivity of LC₅₀=4 ng/cm². Thus, its sensitivity for Bt2 had increased as compared to the reference strain (LC₅₀=20 ng/cm²).

The Bt2/Bt18 selected strain showed a slight but statistically non-significant decrease in Bt18 binding site concentration. (Bt2 : Kd = 0.4 nM, Rt=3.4 pmol/mg vesicle protein, Bt18 : Kd1=0.04 nM, Rt1=1.0 pmoles/mg vesicle protein and Kd2=168nM, Rt2=194 pmoles/mg vesicle protein; 2 distinct receptor sites for Bt18 are present). These data demonstrate that, in the two selection lines where resistance occurred, the mechanism was situated at the receptor level. Changes in receptor site are shown to be the most likely mechanism of resistance to *B. thuringiensis* ICPs.

EXAMPLE 8: Mechanism of resistance of the diamondback moth to the microbial insecticide *Bacillus thuringiensis*.

The mechanism of development of insect resistance to 1cps has been investigated in a *P. xylostella* strain ("PxR"). This insect strain has developed a high level of resistance in the field against Dipel. Crystals of Dipel preparations contain a mixture of ICPs such as Bt3, Bt2 and Bt73 ICPs; in Example 6, it has been shown that these toxins are competitively binding ICPs.

Resistance to Dipel was confirmed by the toxicity data for the sensitive strain ("PxS") and for the Dipel-resistant strain ("PxR"). High levels of resistance are also observed for the Bt2 protoxin and toxin as shown in the following table :

	LC ₅₀ of Strains	
	PxS	PxR
Bt2	6.7	> 1350
Bt15	132.6	120.4

LC₅₀ data are expressed as ng protein spotted per cm² of artificial diet.

However, insect toxicity data show that there is no resistance to the Bt15 protoxin and Bt15 toxin; this ICP

is not present in Dipel crystals. To investigate whether a change in toxin-membrane binding was responsible for resistance, receptor binding studies were performed with ^{125}I -labeled Bt2 toxin and Bt15 toxin, with BBMV derived from larvae midguts of the PxR and PxS strains. The results are summarized in Table 1, below.

ICP	strain	Kd (nM)	Rt (pmol/ mg protein)
Bt2 toxin	PxS	8.1	1.6
	PxR	no binding detectable	
Bt15 toxin	PxS	1.9	4.2
	PxR	3.7	5.8

Table 1 shows that there was high-affinity saturable binding of the Bt2 toxin to midgut membranes of the PxS strain, but the PxR strain showed no detectable level of Bt2 toxin binding. With the Bt15 toxin, there was significant binding to BBMV of both the PxR and PxS strains, and values are not significantly different for the two strains.

These data show that resistance in *P. xylostella* is due to an alteration in toxin-membrane binding. Resistance to the Bt2 toxin and the sensitivity toward the Bt15 toxin of the PxR strain is reflected by the binding characteristics shown in Table 1.

Hence, when different non-competitively binding ICPs (i.e., Bt2 and Bt15) are available with activity against the same insect species (e.g., *P. xylostella*), resistance to one ICP (Bt2) does not imply resistance against other ICPs (such as Bt15). Thus, ICPs with different binding properties can be used in combination to delay development of insect resistance to ICPs.

EXAMPLE 9: Separate transfer of two ICP genes within individual transcriptional units to the genome of plant cells

Two procedures are envisaged for obtaining the combined expression of two ICP genes, such as the *bt2* and *bt15* genes in transgenic plants, such as tomato plants. These procedures are based on the transfer of two chimeric ICP genes, not linked within the same DNA fragment, to the genome of a plant of interest.

A first procedure is based on sequential transformation steps in which a plant, already transformed with a first chimeric ICP gene, is retransformed in order to introduce a second ICP gene. The sequential transformation makes use of two different selectable marker genes, such as the resistance genes for kanamycin ("km") and phosphinotricin acetyl transferase ("PPT"), which confers resistance to phosphinotricin. The use of both these selectable markers has been described in De Block et al. (1987).

The second procedure is based on the cotransformation of two chimeric ICP genes on different plasmids in a single step. The integration of both ICP genes can be selected by making use of the two selectable markers conferring resistance to Km and PPT, linked with the respective ICP genes.

For either procedure, a Ti-plasmid vector is used for *Agrobacterium*-mediated transformation of each chimeric ICP gene into plant cells.

Plasmid PGSH163, described in EP 0193259, contains the following chimeric genes between the T-DNA border repeats: a gene fragment encoding the toxin part of the *bt2* gene under the control of the TR2' promoter and the *neo* gene under control of the TR1' promoter. The 3' ends of the T-DNA gene 7 and octopine synthase respectively provide information for the 3' end formation of transcripts.

A chimeric *bt15* gene containing a gene fragment encoding the toxin of the Bt15 ICP under the control of the TR2' promoter, was constructed in the following way (Figure 15). pOH50 consists of pUC18 with the whole *bt15* gene under the control of the lac promoter. A HindIII-BglII fragment was cloned in pMa5-8 yielding pJB3. By site-directed mutagenesis, a NcoI site was created at the initiation codon to yield pVE29. A fragment containing the truncated gene fragment of the *bt15* gene, with a translational stop codon, was obtained by isolation of BclI-ClaI from pOH50 and cloning in PLK91, yielding pHW38. The whole toxin gene fragment was reconstructed under the control of the tac promoter, yielding pVE35, by ligation of a ClaI-PstI fragment from pHW38, a NcoI-ClaI fragment from pVE29 and a NcoI-PstI fragment from pOH48. A truncated *bt15* gene fragment with a NcoI site at the initiation codon was obtained from pVE35 as a 1980 NcoI-BamHI fragment and cloned in pGSJ141, digested with ClaI and BamHI. pGSJ141 has been described in EPA 88402115.5. Ligation of the filled ClaI site to the filled NcoI site yielded a chimeric TR2' - truncated *bt15* - 3'g7 construct (pTVE47). As a selectable marker in this plasmid, the bar gene encoding phosphinotricin acetyl transferase and conferring

resistance to PPT was used. A chimeric bar gene containing the bar gene under the control of the 35S promoter and followed by the 3' end of the octopine synthase was introduced in pTVE47. From pDE110, a 35S-bar-3'ocs fragment was obtained as a *stul*-HindIII fragment and was cloned in pTVE47 digested with PstI and HindIII. This yielded the plasmid pTHW88 (Figure 15) which contains the truncated *bt15* gene under the control of the TR2' promoter and the bar gene under the control of the 35S promoter between the T-DNA border repeats. Plasmid pGSH163 is cointegration type Ti-plasmid vector, whereas pTHW88 is a binary type Ti-plasmid vector as described in EPA 0193259.

Both plasmids were mobilized in the *A. tumefaciens* strain C58C1RiF (pGV2260) according to Deblaere et al. (1988). In the sequential transformation procedure, tomato was transformed according to De Block et al. (1987) with the *A. tumefaciens* strain C58C1RiF carrying pGS1163 resulting from the cointegration of pGSH163 and pGV2260. Individual transformants were selected for kanamycin resistance, and regenerated plants were characterized for expression of the truncated *bt2* gene according to Vaeck et al. (1987). One representative transformant was subsequently retransformed with the *A. tumefaciens* strain C58C1RiF (pGV2260 and pTHW88), and transformants were selected for PPT resistance. Using this cotransformation procedure, the respective *Agrobacteria* strains, carrying the cointegrate vector pGS1163 and the binary vector pTHW88, were used for transformation of tomato. Individual plants were selected for resistance to Km and PPT.

Schematically shown in Fig. 15 are:

- a) construction of pVE29: *bt15* N-terminal gene fragment with NcoI site introduced at ATG initiation codon.
- b) construction of pVE35: *bt15* C-terminal truncated gene fragment under control of the *tac* promoter.
- c) construction of pTHW88: binary T-DNA vector with a chimeric *bt15* gene and a chimeric *bar* gene within the T-DNA border repeats.

In both cases, co-expression of the two ICP genes in the individual transformants was evaluated by insect toxicity tests as described in EP 0193259 and by biochemical means. Specific RNA probes allowed the quantitative analysis of the transcript levels; monoclonal antibodies cross-reacting with the respective gene products allowed the quantitative analysis of the respective gene products in ELISA tests (EP 0193259); and specific DNA probes allowed the characterization of the genomic integrations of the *bt2* and *bt15* genes in the transformants. It was found that the transformed tomato plants simultaneously expressed both the *bt2* gene (8.1 ng/mg) and the *bt15* gene (7.6 ng/mg) as measured by ELISA, which would prevent or delay development of resistance of *M. sexta* to the insecticidal effects of the Bt2 and Bt15 toxins, being expressed.

These procedures also could be applied when one or both ICP genes are part of a hybrid gene. For example, the same strategy as described above could be followed with the plasmid vectors pGSH152, containing a chimeric truncated *bt2-neo* hybrid gene under control of the TR2' promoter, and pTHW88 in suitable *Agrobacterium* strains.

EXAMPLE 10: Separate transfer of two ICP genes to the nuclear genome of separate plants in independent transformation events and subsequent combination in a single plant through crossing.

Tobacco plants have been transformed with either the *bt18* gene or the *bt15* gene by applying the same cloning strategies as described in EP 0358557 and EP 193259, respectively. For both genes, the plants were transformed with plant expression vectors containing either the truncated *bt18* or *bt15* gene, which just encode the Bt18 or Bt15 toxin, respectively.

The mortality rate of *Spodoptera littoralis* larvae feeding on the transformed plants is significantly higher than the mortality rate of larvae fed on untransformed plants.

The *bt18*-transformed plant, which is homozygous for the *bt18* gene, is then crossed with the *bt15*-transformed plant, which is homozygous for the *bt15* gene. After selfing, a plant homozygous for both genes is obtained.

The resulting tobacco plants, expressing both the *bt18* and *bt15* genes, delay significantly development of resistance by *S. littoralis* to either the Bt18 or Bt15 toxin expressed by the plants.

EXAMPLE 11: Transfer of two chimeric ICP genes linked within the same DNA to the genome of plant cells

The strategy used is based on the organization of two independent chimeric ICP genes between the T-DNA border repeats of a single vector. Binding studies indicated that the Bt2 and Bt14 toxins are two non-competitively binding ICPs with insecticidal activity towards *Pieris brassicae*. For expression in plants, both the *bt2* and *bt14* genes can be co-expressed to prevent insect resistance development. For the design of a plasmid

vector with each ICP gene under the control of a separate promoter, two possibilities can be envisaged: 1) three chimeric constructs carrying the truncated bt2 and bt14 genes and a selectable marker, respectively; or 2) a hybrid of a truncated gene fragment (bt2 or bt14) and the neo gene can be used in combination with a truncated bt14 or bt2 gene.

This Example describes the construction of the vector pTHW94 for plant transformations carrying the following chimeric ICP genes between the T-DNA border repeats: a truncated bt2 gene fragment under the control of the TR2' promoter and a hybrid truncated bt14-neo gene under the control of the TR1' promoter. The 3' end of the T-DNA gene 7 and octopine synthase, respectively, provide information for proper 3' end formation. pTHW94 has been deposited at the DSM under accession no. 5514 on August 28, 1989.

Schematically shown in Fig. 16 are the:

- a) construction of pHW44: bt14 N-terminal gene fragment with NcoI site introduced at ATG initiation codon.
- b) construction of pHW67: reconstruction of the bt14 gene under the control of the tac promoter.
- c) construction of pHW71: construction of a hybrid truncated bt14-neo gene under the control of the tac promoter.
- d) construction of pTHW94: binary T-DNA vector with chimeric bt14 gene and a chimeric bt2 gene within the T-DNA border repeats.

The pTHW94 vector is mobilized into the *Agrobacterium* strain C58C1RiF (pMP90) which is used to transform *Brassica napus* according to the procedure described by De Block et al. (1989). Transformants are selected on Km, and regenerated plants are found to express both ICP gene products in insect toxicity tests and biochemical tests.

EXAMPLE 12: Expression of two ICP genes in a hybrid construct

In order to obtain a combined and simultaneous expression of two ICP genes, truncated gene fragments encoding the toxic parts of two different ICPs can be fused in a proper reading frame and placed, as a hybrid gene, under the control of the same promoter in a chimeric gene construct. Toxic cores from certain ICPs can be liberated from their protoxins by protease activation at the N- and/or C- terminal end. Thus, hybrid genes can be designed with one or more regions encoding protease cleavage site(s) at the fusion point(s) of two or more ICP genes.

The simultaneous co-expression of the bt2 and bt14 genes is obtained by constructing a hybrid gene composed of a truncated bt14 gene fragment fused to a truncated bt2 gene fragment. Schematically shown in Figure 17 is the construction of such a hybrid bt2-bt14 gene with a C-terminal bt2 gene fragment (bt860) encoding the toxic core of the Bt2 protoxin in frame with a C-terminal truncated bt14 gene fragment encoding the toxic core of the Bt14 protoxin. The BclI site in the bt2 gene, localized downstream of the trypsin cleavage site, is fused in frame with the NcoI site introduced at the N-terminal end of the truncated bt14 gene fragment. To this end, the plasmids pLBKm860 (EP 0193259) and pHW67 are used. pLBKm860 contains a hybrid bt2-neo gene under control of the lambda P_L promoter. The bt2 gene moiety in the hybrid gene is a C-terminal truncated bt2 gene fragment, indicated as bt860 (in Fig. 17) (see also Vaeck et al, 1987). The construction of pHW67 is described in Fig. 16. pHW67 contains a C-terminal truncated bt14 gene fragment (bt14tox) with a NcoI site at the ATG initiation codon, a translation stop codon located at the BclI site of the intact bt14 gene and a BamHI site downstream of the whole gene fragment. To fuse both gene fragments in the proper reading frame, the BclI and NcoI ends of the respective plasmids are treated with Klenow DNA polymerase and S1 nuclease as indicated in Figure 16. The resulting plasmid pJB100 contains the hybrid bt860-bt14tox gene under control of the lambda P_L promoter and directs the expression in *E. coli* of a fusion protein with the expected mobility on SDS-PAGE.

Crude extracts of the *E. coli* strain show the toxicity of the fusion protein, expressed by the strain, against *P. brassicae*. It has also been confirmed by N-terminal amino acid sequence analyses of the fusion protein produced by the *E. coli* strain that the N-terminal amino acids from the Bt14 protoxin are processed upon activation. The bt2-bt14 hybrid gene product has thus two potential protease cleavage sites.

Subsequently, this hybrid gene is inserted into a vector for plant transformations and placed under control of a suitable promoter and transferred to the genome of brassica (EP 0193259) where both the bt2 and bt14 genes are expressed in insect toxicity tests.

Table 2

Gene	Bt strain	Host range	amino acids encoded	predicted MW(kDa) of encoded aminoacids	Disclosure of nucleotide sequence
bt3	HD-1 kurstaki	L	1176	133.2	Schnepf et al., 1985
bt2	berliner 1715	L	1155	131	Höfte et al., 1986
bt73	HD-73	L	1178	133.3	Adang et al, 1985
bt14	entomocidus HD-110	L	1207	138	Brizzard and Whiteley, 1988
bt15	entomocidus HD-110	L	1189	134.8	Fig. 14
bt4	HD-68 aizawai	L	1165	132.5	Fig. 13
bt18	darmstadiensis HD-146	L	1171	133	EP appln. 88402241.9
bt13	Bt51, DSM4288 22/10/87	C	644	73.1	EP appln. 88402115.5
bt21	BtPGSI208, DSM 5131, 19/1/89	C	651	74.2	EP appln. 89400428.2
bt22	BtPGSI245, DSM 5132, 19/1/89	C	1138	129	EP appln. 8940028.2
p2	HD-263	L/D	633	70.9	Donovan et al. 1988
Cry B2	HD-1	L	633	70.8	Widner and Whiteley, 1989

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Claims

1. Cells of a plant, characterized by: at least two B. thuringiensis Insecticidal Crystal Protein genes stably inserted into the genome of said plant; said genes being under the control of the same or distinct promoter and each of said genes encoding a different non-competitively binding Insecticidal Crystal Protein for the same insect species; whereby at least two different Insecticidal Crystal Proteins can be produced in cells of said plant.
- 40 2. Cells of Claim 1 wherein at least one marker gene, encoding a protein or polypeptide which renders said cells easily distinguishable from cells which do not contain said protein or polypeptide, is in the same genetic locus as at least one of said Insecticidal Crystal Protein genes.
- 45 3. Cells of Claim 1 or 2, wherein each of said Insecticidal Crystal Protein genes is under the control of a separate promoter capable of directing gene expression in said cells and is provided with a separate signal for 3' end formation and within a same transcriptional unit.
- 50 4. Cells of Claim 2 or 3, in which said marker gene is under the control of a separate promoter capable of directing gene expression in said plant cells and is provided with a signal for 3' end formation within a same transcriptional unit.
- 55 5. Cells of Claim 1 or 2, wherein said Insecticidal Crystal Protein genes are within a same transcriptional unit and under the control of a single promoter.

6. Cells of Claim 5, wherein said marker gene is fused with at least one of said Insecticidal Crystal Protein genes and is within said same transcriptional unit and under the control of said promoter.
- 5 7. Cells of Claim 5 or 6, wherein a DNA fragment, encoding a protease-sensitive or - cleavable amino acid sequence, is in said same transcriptional unit as said Insecticidal Crystal Protein genes and intercalated in frame between said Insecticidal Crystal Protein genes.
8. Cells of Claim 5 or 6, wherein said Insecticidal Crystal Protein genes are combined in a dicistronic unit comprising an intergenic DNA sequence which allows reinitiation of translation and is in said same trans-
10 scriptional unit as said Insecticidal Crystal Protein genes and intercalated between said Insecticidal Crystal Protein genes.
9. Cells of any one of Claims 1 to 8, wherein said Insecticidal Crystal Protein genes are encoding insecticidal proteins having activity against Lepidoptera species and are particularly the following genes: bt2 and/or bt73 and/or bt4 and/or bt14 and/or bt15 and/or bt18.
15
10. Cells of any one of Claims 1 to 8, wherein said Insecticidal Crystal Protein genes are genes encoding insecticidal proteins having activity against a Coleoptera species and are particularly the following genes: bt13 and/or bt21 and/or bt22.
- 20 11. Cells of any one of Claims 2 to 10 wherein said marker gene is: a herbicide resistance gene, particularly a sfr or sfrv gene; a gene encoding a modified target enzyme for a herbicide having a lower affinity for the herbicide, particularly a modified 5-EPSP as a target for glyphosate or a modified glutamine synthetase as a target for a GS inhibitor; or an antibiotic resistance gene, particularly NPTII.
- 25 12. Cells of any one of Claims 1 to 11, wherein any of said same or distinct promoters of said Insecticidal Crystal Proteins are selected from the group of: a constitutive promoter, particularly a 35S promoter or a 35S3 promoter; a PNOS promoter; a POCS promoter; a wound-inducible promoter, particularly a TR1' or TR2' promoter; a promoter which directs gene expression selectively in plant tissue having photosynthetic activity, particularly a SSU promoter; or a tissue-specific or an organ specific promoter, particularly
30 a tuber-specific promoter, a stem-specific promoter or a seed-specific promoter or an inducible promoter, particularly a promoter induced by chemical factors or temperature or combinations thereof.
13. A vector suitable for transforming cells of a plant, particularly a plant capable of being infected with Agrobacterium, comprising said Insecticidal Crystal Protein genes of any one of Claims 1 to 12.
35
14. A process for producing a plant having improved insect resistance and having said Insecticidal Crystal Protein gene combinations of any one of Claims 1 to 12 stably integrated into the nuclear genome of its cells, characterized by the non-biological steps of transforming a plant cell by introducing the Insecticidal Crystal Protein gene combinations of any one of Claims 1 to 12 into the nuclear genome of said cell and
40 regenerating said plant and reproduction material from said cell.
15. A plant cell culture, consisting of the plant cells of any one of Claims 1 to 12.
16. A plant, consisting of the plant cells of any one of Claims 1 to 12.
- 45 17. Brassica, tomato, potato, tobacco, cotton or lettuce consisting of the plant cells of any one of Claims 1 to 12, wherein said Insecticidal Crystal Protein genes comprise one of the following pairs of genes: bt2 and bt18 or bt73 and bt15 or bt2 and bt18 or bt2 and bt14 or bt2 and bt4 or bt15 and bt18 or bt14 and bt15 or bt4 and bt15 or bt13 and bt21 or bt21 and bt22 or bt13 and bt22.
- 50 18. A method for rendering a plant resistant to an insect species by transforming the plant with said Insecticidal Crystal Protein genes of any one of Claims 1-12.
19. A plant characterized by: at least two B. thuringiensis Insecticidal Crystal Protein genes stably inserted into the genome of said plant; said genes being under the control of the same or distinct promoter and
55 each of said genes encoding a different non-competitively binding Insecticidal Crystal Protein for the same insect species; whereby at least two different Insecticidal Crystal Proteins can be produced in cells of said plant.

20. Cells of a plant according to Claim 1 wherein said B. thuringiensis Insecticidal Crystal Protein genes have naturally occurring or synthetic nucleotide sequences.

5 Patentansprüche

1. Pflanzenzellen, dadurch gekennzeichnet, daß wenigstens zwei B. thuringiensis insecticidal crystal protein - Gene stabil in das Genom dieser Pflanze eingesetzt sind, diese Gene der Kontrolle desselben oder eines jeweils bestimmten Promoters unterliegen und jedes dieser Gene ein anderes, ohne wechselseitige Be-
10 einflussung eingebundenes insecticidal crystal protein verschlüsselt, wobei die wenigstens zwei Insecticidal crystal proteine in Zellen dieser Pflanzen erzeugt werden können.
2. Zellen nach Anspruch 1, wobei wenigstens ein Markierungsgen, das ein Protein oder Polypeptid verschlüsselt, das diese Zellen leicht von den Zellen unterscheiden läßt, die dieses Protein oder Polypeptid
15 nicht enthalten, sich an derselben genetischen Stelle befindet wie wenigstens eines dieser insecticidal crystal protein - Gene.
3. Zellen nach Anspruch 1 oder 2, wobei jedes dieser insecticidal crystal protein - Gene der Kontrolle eines anderen Promoters unterliegt, der die Umsetzung der Gene in diesen Zellen steuern kann und mit einem getrennten Signal für 3' - Endbildung innerhalb derselben Transcriptase-Einheit versehen ist.
20
4. Zellen nach Anspruch 2 oder 3, wobei jedes der Markierungsgene der Kontrolle eines anderen Promoters unterliegt, der die Umsetzung der Gene in diesen Zellen steuern kann und mit einem getrennten Signal für 3' - Endbildung innerhalb derselben Transcriptase-Einheit versehen ist.
- 25 5. Zellen nach Anspruch 1 oder 2, wobei diese insecticidal crystal protein sich in derselben Transcriptase-Einheit befinden und einem Promoter unterliegen.
6. Zellen nach Anspruch 5, wobei das Markierungsgen mit wenigstens einem der insecticidal crystal protein - Gene verbunden ist, sich in derselben Transcriptase-einheit befindet und der Kontrolle desselben Promoters unterliegt.
30
7. Zellen nach Anspruch 5 oder 6, wobei ein DNA-Bruckstück, das eine protease-empfindliche oder protease-gebundene Aminosäuresequenz verschlüsselt, sich in derselben Transcriptase-Einheit wie die insecticidal crystal protein - Gene befindet und in den Rahmen zwischen den insecti-cidal crystal protein - Genen eingeschoben ist.
35
8. Zellen nach Anspruch 5 oder 6, wobei diese Insecticidal crystal protein - Gene in einer dicistronischer Einheit zusammengefaßt sind, die eine zwischengenetische DNA-Sequenz umfaßt, die einen erneuten Beginn der Übersetzung erlaubt und sich in derselben Transcriptase-Einheit wie die insecticidal crystal protein - Gene befindet und zwischen diese insecticidal crystal protein - Gene eingeschoben ist.
40
9. Zellen nach einem der Ansprüche 1 - 8, wobei die insecticidal crystal protein - Gene insecticidal Proteine verschlüsseln, die Aktivität gegen Lepidoptera-Spezien entfalten und besonders die folgenden Gene sind: bt2 und/oder bt73 und/oder bt4 und/oder bt14 und/oder bt15 und/oder bt18 .
45
10. Zellen nach einem der Ansprüche 1 - 8, wobei die insecticidal crystal protein - Gene insecticidal Proteine verschlüsseln, die Aktivität gegen eine Coleoptera-Spezies entfalten und besonders die folgenden Gene sind: bt13 und/oder bt21 und/oder bt22
- 50 11. Zellen nach einem der Ansprüche 2 - 10, wobei das Markierungsgen ein herbizidresistentes Gen ist, insbesondere ein sfr oder sfrv Gen, oder ein Gen ist, das ein verändertes Zielenzym für ein Herbizid mit geringerer Empfindlichkeit gegenüber diesem Herbizid verschlüsselt, insbesondere ein verändertes 5-EPSP als Ziel für Glyphosat oder eine veränderte Glutamin-Synthetase als Ziel für einen GS-Hemmer, oder ein gegen Antibiotika resistentes Gen ist, insbesondere NPTII.
- 55 12. Zellen nach einem der Ansprüche 1 - 11, wobei jeder beliebige dieser gleichen oder jeweils bestimmten Promoter dieser insecticidal crystal proteine aus einer Gruppe ausgewählt ist, die sich zusammensetzt aus einem angeborenen Promoter, insbesondere einem 35S oder 35S3 Promoter, einem PNOS Promoter,

- 5 einem durch Verletzung einführbaren Promoter, insbesondere einem TR1' oder TR2' Promoter, einem Promoter, der die Entfaltung der Gene gesteuert in Pflanzengewebe mit photosynthetischer Aktivität richtet, insbesondere einem SSU Promoter, oder einem gewebe- oder organspezifischen Promoter, insbesondere einem knollenspezifischen Promoter, einem stengel- oder samenspezifischen Promoter, oder einem einführbaren Promoter, insbesondere einem Promoter, der durch chemische Faktoren oder Temperatur oder Kombinationen davon einführbar ist.
- 10 13. Ein Bakterienüberträger geeignet zur Veränderung von Pflanzenzellen, insbesondere einer Pflanze, die mit Agrobacterium infiziert werden kann, der die insecticidal crystal protein - Gene nach einem der Ansprüche 1 - 12 enthält.
- 15 14. Verfahren zur Erzeugung einer Pflanze, die eine erhöhte Widerstandsfähigkeit gegen Insekten besitzt und stabil in das Kerngenom ihrer Zellen eingesetzte insecticidal crystal protein - Genkombinationen nach einem der Ansprüche 1 - 12 aufweist, gekennzeichnet durch die nichtbiologischen Schritte der Veränderung einer Pflanzenzelle durch Einführen der insecticidal crystal protein - Genkombination nach einem der Ansprüche 1 - 12 in das Kerngenom dieser Zelle und das Wiederherstellen dieser Pflanze und des Vermehrungsmaterials ausgehend von dieser Zelle.
- 20 15. Eine Pflanzenzellenkultur, bestehend aus Pflanzenzellen nach einem der Ansprüche 1 - 12.
16. Eine Pflanze, bestehend aus Pflanzenzellen nach einem der Ansprüche 1 - 12.
- 25 17. Kohl, Tomaten, Kartoffeln, Tabakpflanzen, Wollpflanzen oder Salat, bestehend aus den Pflanzenzellen nach einem der Ansprüche 1 - 12, wobei die insecticidal crystal protein - Gene eines der folgenden Genpaare umfassen: bt2 und bt18 oder bt73 und bt15 oder bt2 und bt18 oder bt2 und bt14 oder bt2 und bt4 oder bt15 oder bt18 oder bt14 und bt15 oder bt4 und bt15 oder bt13 und bt21 oder bt21 und bt22 oder bt13 und bt22.
- 30 18. Verfahren zur Resistenzherstellung einer Pflanze gegen eine Insektenart durch Veränderung der Pflanze mit den insecticidal crystal protein - Genen nach einem der Ansprüche 1 - 12.
- 35 19. Pflanze, gekennzeichnet durch wenigstens zwei stabil in das Genom dieser Pflanze eingefügte B. thuringiensis insecticidal crystal protein - Gene, wobei diese Gene der Kontrolle desselben oder eines jeweils bestimmten Promotors unterliegen und jedes dieser Gene ein anderes, ohne Beeinflussung eingebundenes insecticidal crystal protein für dieselbe Insektenart verschlüsselt, wobei wenigstens zwei verschiedene insecticidal crystal proteins in den Zellen dieser Pflanze erzeugt werden können.
20. Pflanzenzellen nach Anspruch 1, wobei die B. thuringiensis insecticidal crystal protein - Gene natürlich vorkommende oder synthetische Kernfolgen aufweisen.

Revendications

- 45 1. Cellules d'une plante, caractérisées par au moins deux gènes de protéine cristalline insecticide de B. thuringiensis insérés de façon stable dans le génome de cette plante; ces gènes étant sous le contrôle du même promoteur ou de promoteurs distincts et chacun de ces gènes codant pour une protéine cristalline insecticide différente se liant de façon non compétitive pour la même espèce d'insecte; de telle sorte qu'au moins deux protéines cristallines insecticides différentes peuvent être produites dans des cellules de cette plante.
- 50 2. Cellules suivant la revendication 1, dans lesquelles au moins un gène marqueur, codant pour une protéine ou un polypeptide permettant à ces cellules d'être facilement distinguées d'autres cellules qui ne contiennent pas cette protéine ou ce polypeptide, est dans le même locus génétique qu'au moins l'un de ces gènes de protéine cristalline insecticide.
- 55 3. Cellules suivant les revendications 1 ou 2, dans lesquelles chacun de ces gènes de protéine cristalline insecticide est sous le contrôle d'un promoteur séparé capable de diriger l'expression du gène dans ces cellules et est pourvu d'un signal séparé pour la formation de l'extrémité 3' et dans une même unité transcriptionnelle.

4. Cellules suivant les revendications 2 ou 3, dans lesquelles ce gène marqueur est sous le contrôle d'un promoteur séparé capable de diriger l'expression du gène dans ces cellules végétales et est pourvu d'un signal pour la formation de l'extrémité 3' et dans une même unité transcriptionnelle.
- 5 5. Cellules suivant les revendications 1 ou 2, dans lesquelles ces gènes de protéine cristalline insecticide sont dans une même unité transcriptionnelle et sous le contrôle d'un promoteur unique.
6. Cellules suivant la revendication 5, dans lesquelles ce gène marqueur est fusionné à l'un au moins de ces gènes de protéine cristalline insecticide et est dans cette même unité transcriptionnelle et sous le contrôle de ce promoteur unique.
- 10 7. Cellules suivant les revendications 5 ou 6, dans lesquelles un fragment d'ADN, codant pour une séquence d'acides aminés pouvant être coupée par une protéase ou sensible à une protéase, est dans la même unité transcriptionnelle que ces gènes de protéine cristalline cristalline et est intercalé dans le cadre entre ces gènes de protéine cristalline insecticide.
- 15 8. Cellules suivant les revendications 5 ou 6, dans lesquelles ces gènes de protéine cristalline insecticide sont combinés dans une unité dicistronique comprenant une séquence d'ADN intergénique qui permet une réinitiation de la traduction et est dans la même unité transcriptionnelle que ces gènes de protéine cristalline cristalline et intercalée entre ces gènes de protéine cristalline insecticide.
- 20 9. Cellules suivant l'une quelconque des revendications 1 à 8, dans lesquelles ces gènes de protéine cristalline cristalline codent pour des protéines insecticides ayant une activité contre des espèces de Lepidoptera et sont en particulier les gènes suivants : bt2 et/ou bt73 et/ou bt4 et/ou bt14 et/ou bt15 et/ou bt18.
- 25 10. Cellules suivant l'une quelconque des revendications 1 à 8, dans lesquelles ces gènes de protéine cristalline cristalline sont des gènes codant pour des protéines insecticides ayant une activité contre une espèce de Coleoptera et sont en particulier les gènes suivants : bt13 et/ou bt21 et/ou bt22.
- 30 11. Cellules suivant l'une quelconque des revendications 2 à 10, dans lesquelles ce gène marqueur est : un gène de résistance à un herbicide, en particulier un gène sfr ou sfrv; un gène codant pour une enzyme cible modifiée pour un herbicide ayant une affinité inférieure pour l'herbicide, en particulier un 5-EPSP modifié comme cible pour un glyphosate ou une glutamine synthétase modifiée comme cible pour un inhibiteur de GS; ou un gène de résistance à un antibiotique, en particulier NPTII.
- 35 12. Cellules suivant l'une quelconque des revendications 1 à 11, dans lesquelles l'un quelconque de ces promoteurs identiques ou distincts de ces protéines cristallines insecticides est sélectionné parmi le groupe comprenant : un promoteur constitutif, en particulier un promoteur 35S ou un promoteur 35S3; un promoteur PNOS, un promoteur POCs; un promoteur pouvant être induit par une plaie, en particulier un promoteur TR1' ou TR2'; un promoteur qui dirige l'expression génique sélectivement dans un tissu végétal ayant une activité photosynthétique, particulièrement un promoteur SSU; ou un promoteur spécifique d'un tissu ou spécifique d'un organe, en particulier un promoteur spécifique d'une tubercule, un promoteur spécifique d'une tige, un promoteur spécifique d'une graine ou un promoteur inductible, en particulier un promoteur induit par des facteurs chimiques ou la température ou leurs combinaisons.
- 40 13. Vecteur convenable pour transformer des cellules d'une plante, en particulier d'une plante pouvant être infectée avec Agrobacterium, comprenant ces gènes de protéine cristalline insecticide de l'une quelconque des revendications 1 à 12.
- 45 14. Procédé pour produire une plante ayant une résistance aux insectes améliorée et ayant ces combinaisons de gènes de protéine cristalline insecticide de l'une quelconque des revendications 1 à 12 intégrées de façon stable dans le génome nucléaire de ses cellules, caractérisé par les étapes non biologiques de transformation d'une cellule végétale par introduction des combinaisons de gènes de protéine cristalline insecticide de l'une quelconque des revendications 1 à 12 dans le génome nucléaire de cette cellule et de régénération de cette plante et du matériel de reproduction à partir de cette cellule.
- 50 15. Culture de cellules végétales, consistant en cellules végétales de l'une quelconque des revendications 1 à 12.
- 55

16. Plante, consistant en cellules végétales de l'une quelconque des revendications 1 à 12.
17. Chou, tomate, pomme de terre, tabac, coton ou laitue, consistant en cellules végétales de l'une quelconque des revendications 1 à 12, dans lesquels ces gènes de protéine cristalline insecticide comprennent l'une des paires de gènes suivantes : bt2 et bt18, ou bt73 et bt15, ou bt2 et bt18, ou bt2 et bt14, ou bt2 et bt4 ou bt15 et bt18, ou bt14 et bt15, ou bt4 et bt15 ou bt13 et bt21, ou bt21 et bt22, ou bt13 et bt22.
18. Méthode pour rendre une plante résistante à une espèce d'insecte par transformation de la plante avec ces gènes de protéine cristalline insecticide de l'une quelconque des revendications 1 à 12.
19. Plante caractérisée par au moins deux gènes de protéine cristalline insecticide de B. thuringiensis insérés de façon stable dans le génome de cette plante; ces gènes étant sous le contrôle du même promoteur ou d'un promoteur distinct et chacun de ces gènes codant pour une protéine cristalline insecticide différente se liant de façon non compétitive pour la même espèce d'insecte; de telle sorte qu'au moins deux protéines cristallines insecticides différentes peuvent être produites dans des cellules de cette plante.
20. Cellules d'une plante suivant la revendication 1, dans lesquelles ces gènes de protéine cristalline insecticide de B. thuringiensis ont des séquences de nucléotides d'origine naturelle ou synthétique.

FIGURE 1

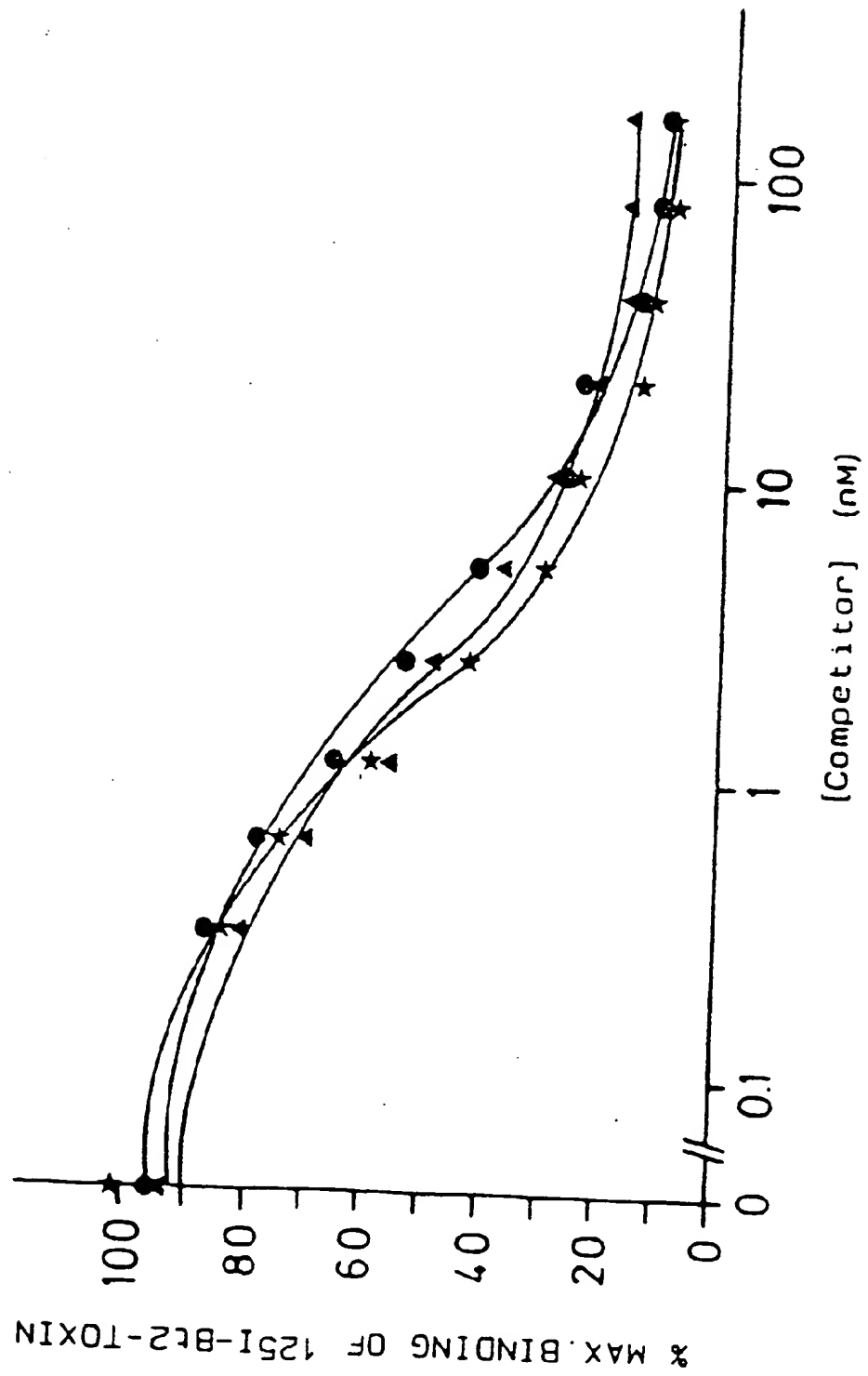


FIGURE 2

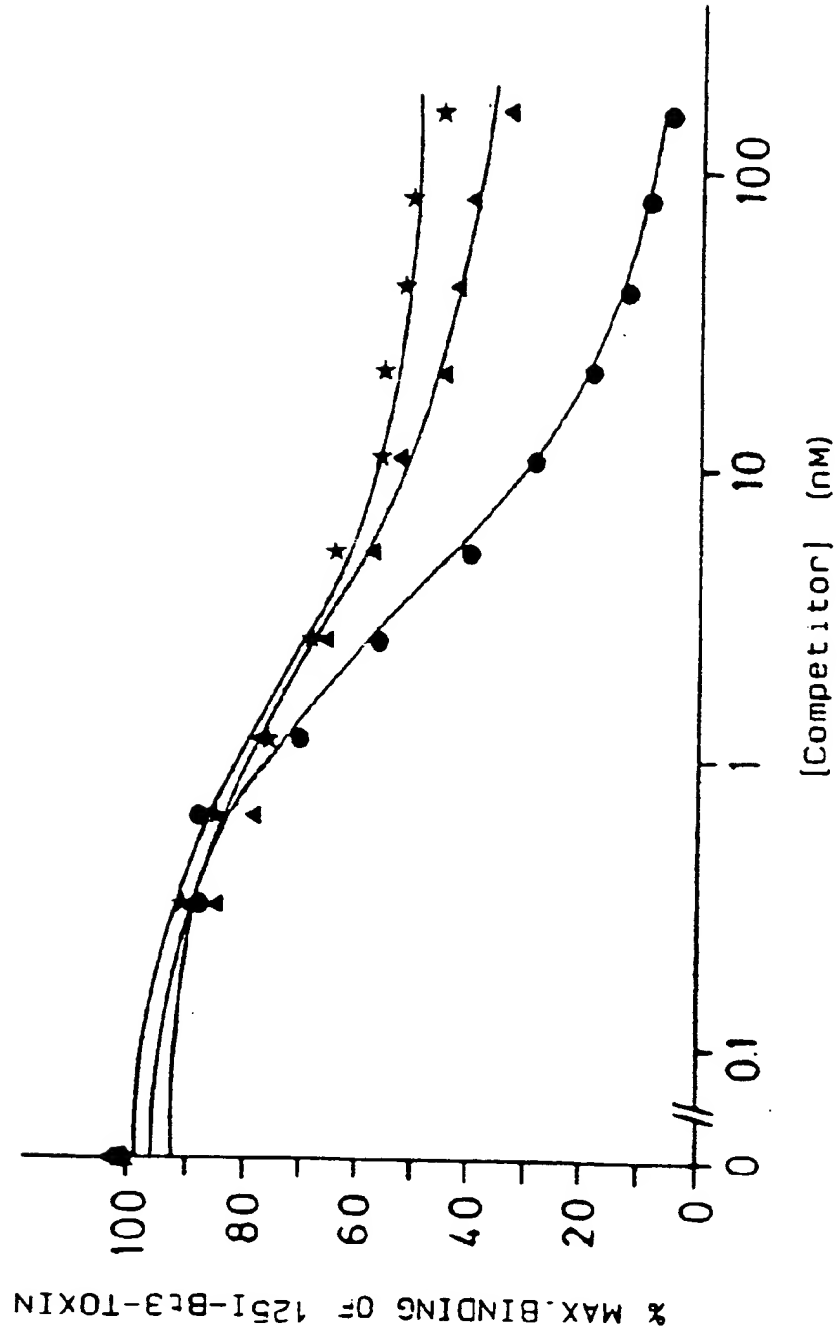


FIGURE 3

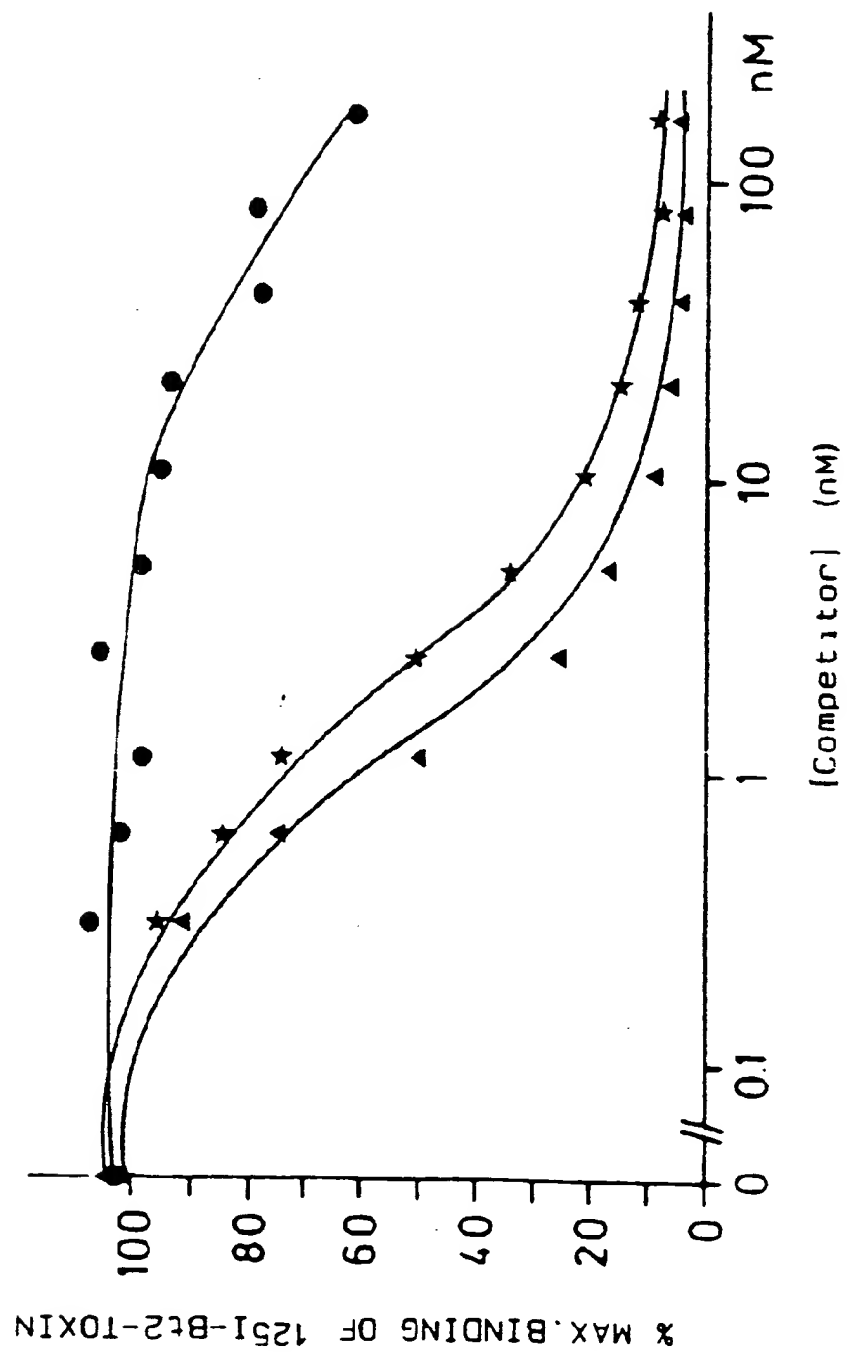


FIGURE 4

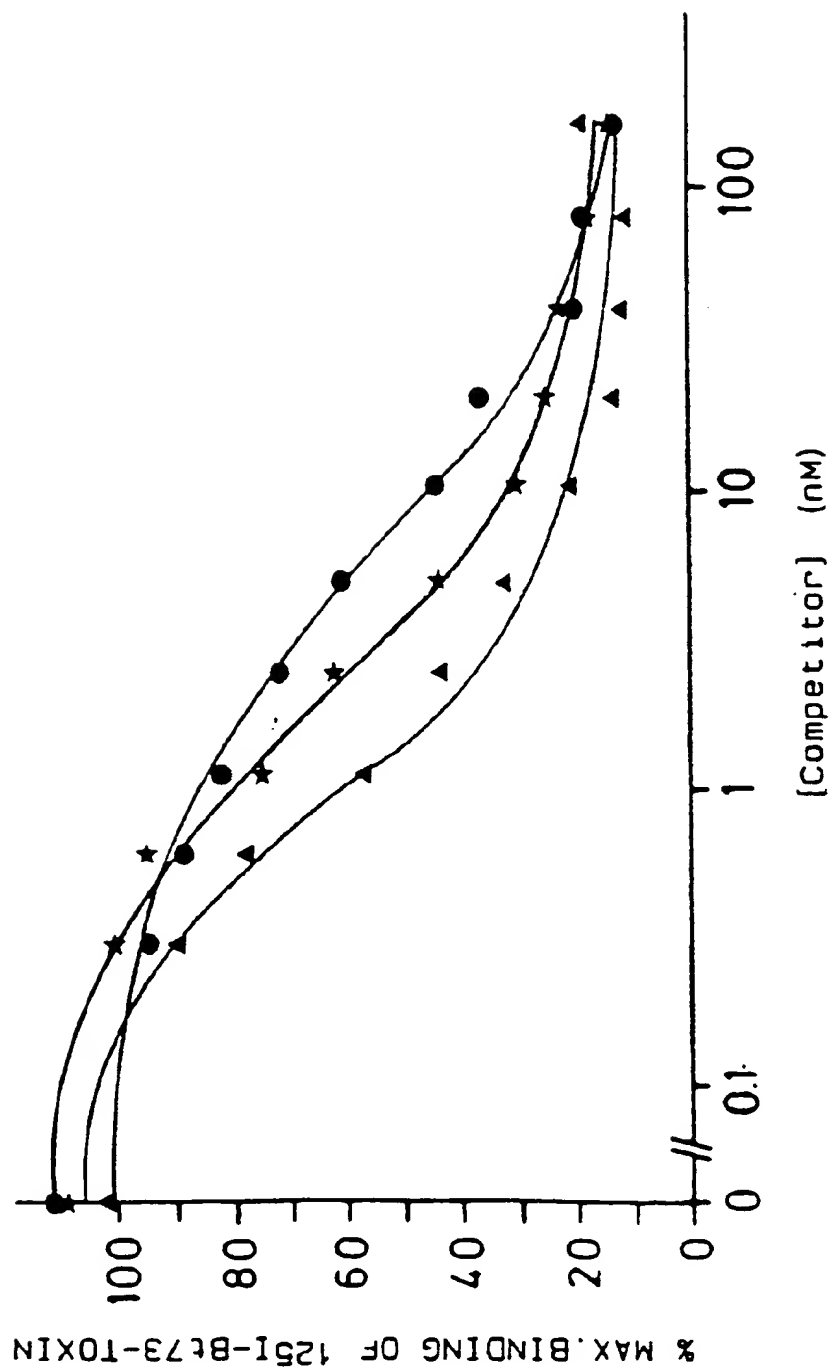


FIGURE 5

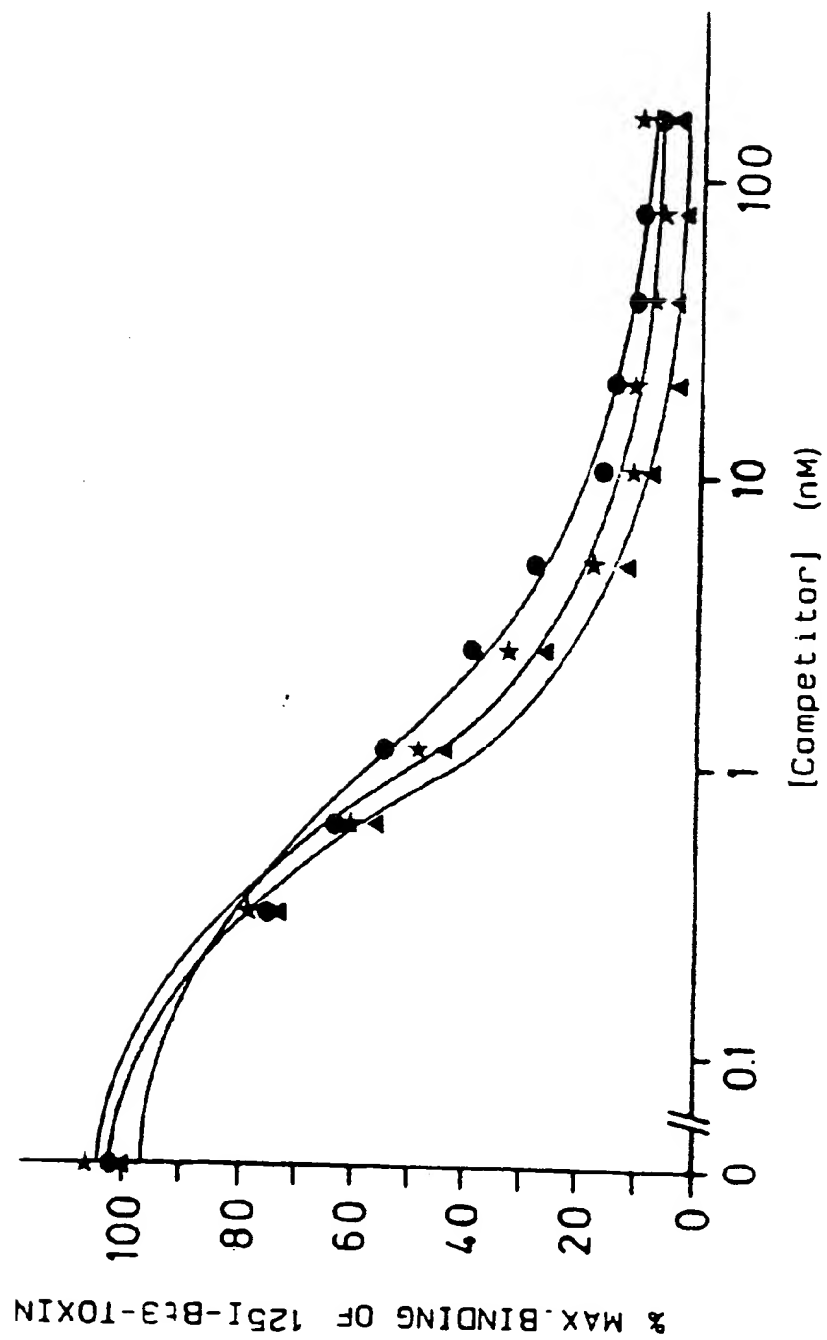


FIGURE 6

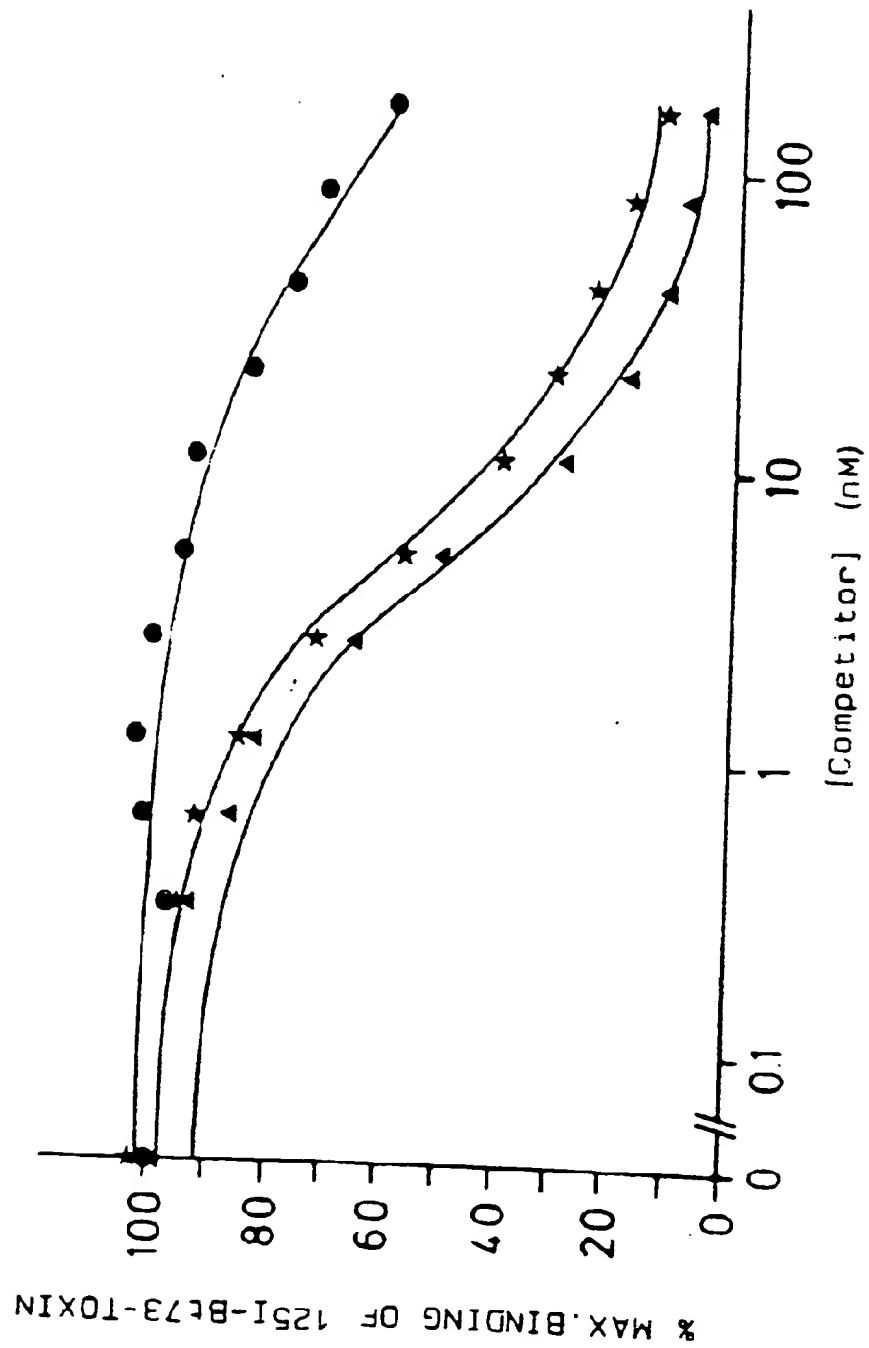
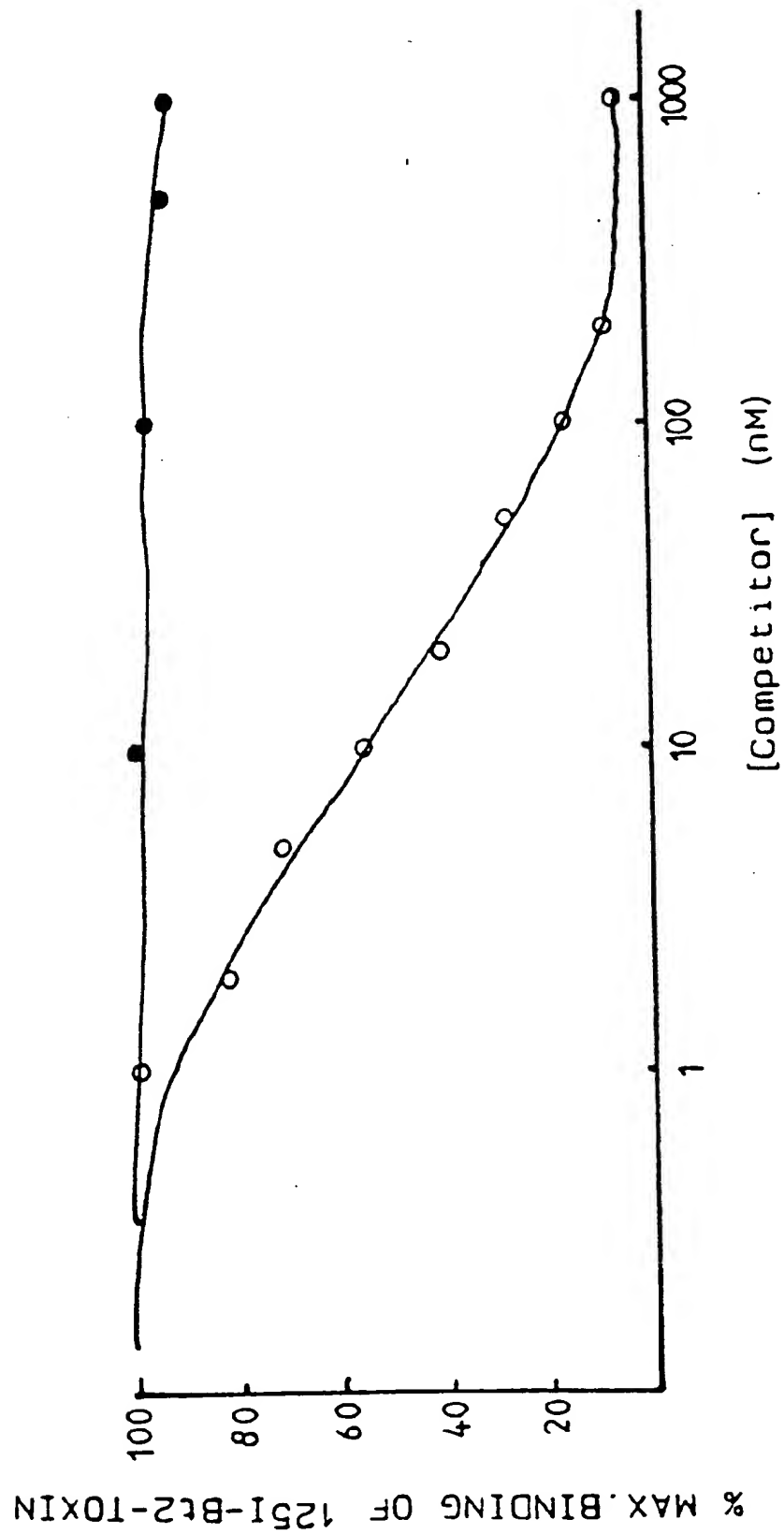


FIGURE 7



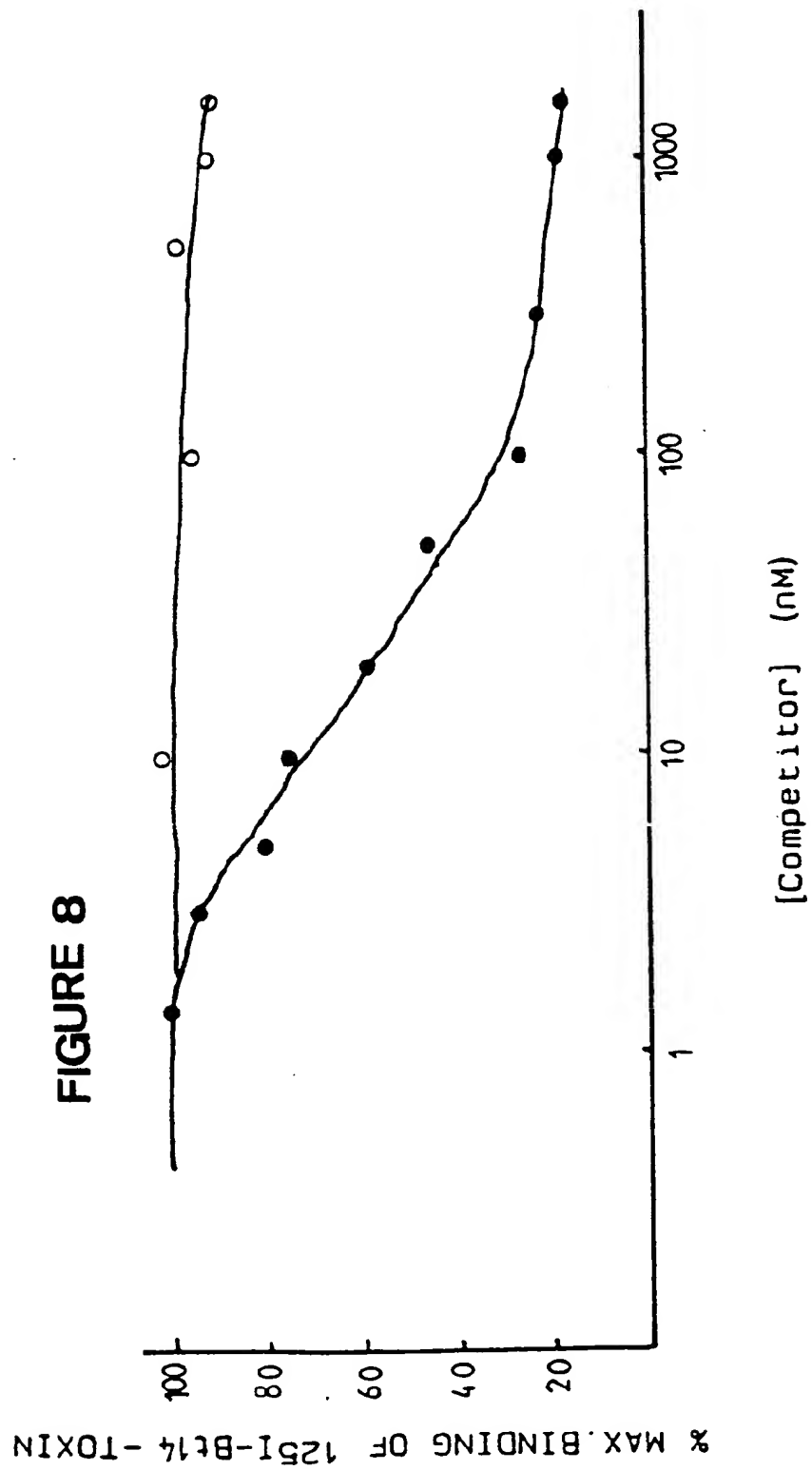


FIGURE 9

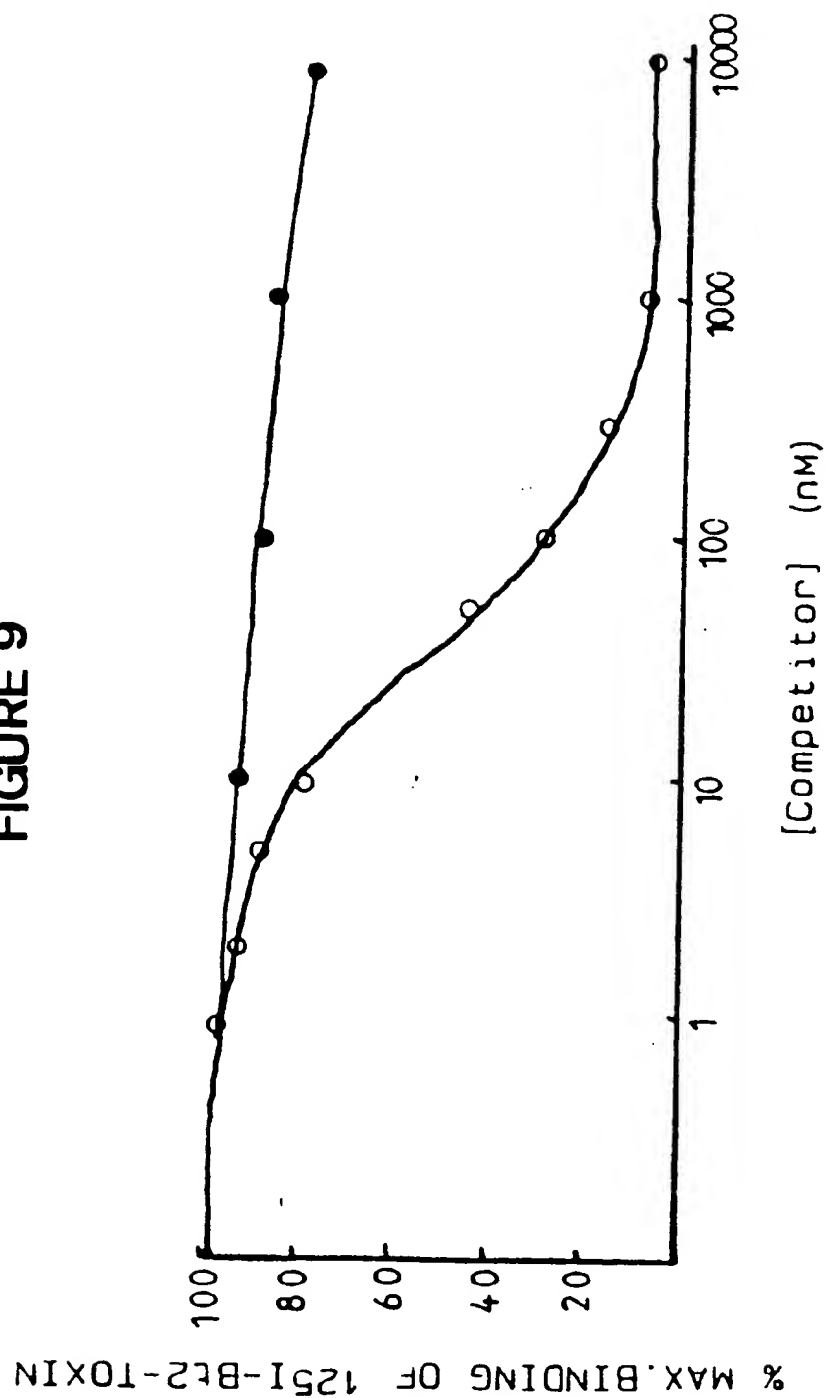


FIGURE 10

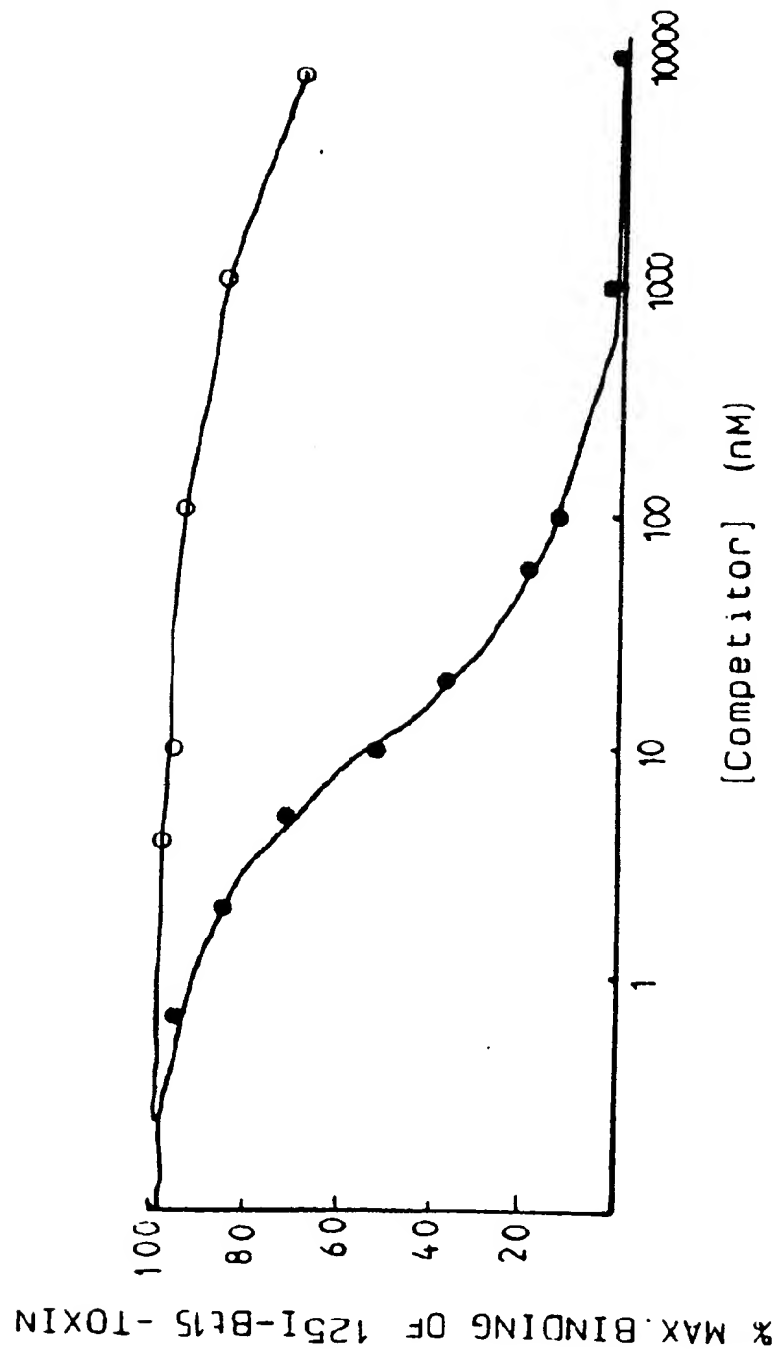


FIGURE 11

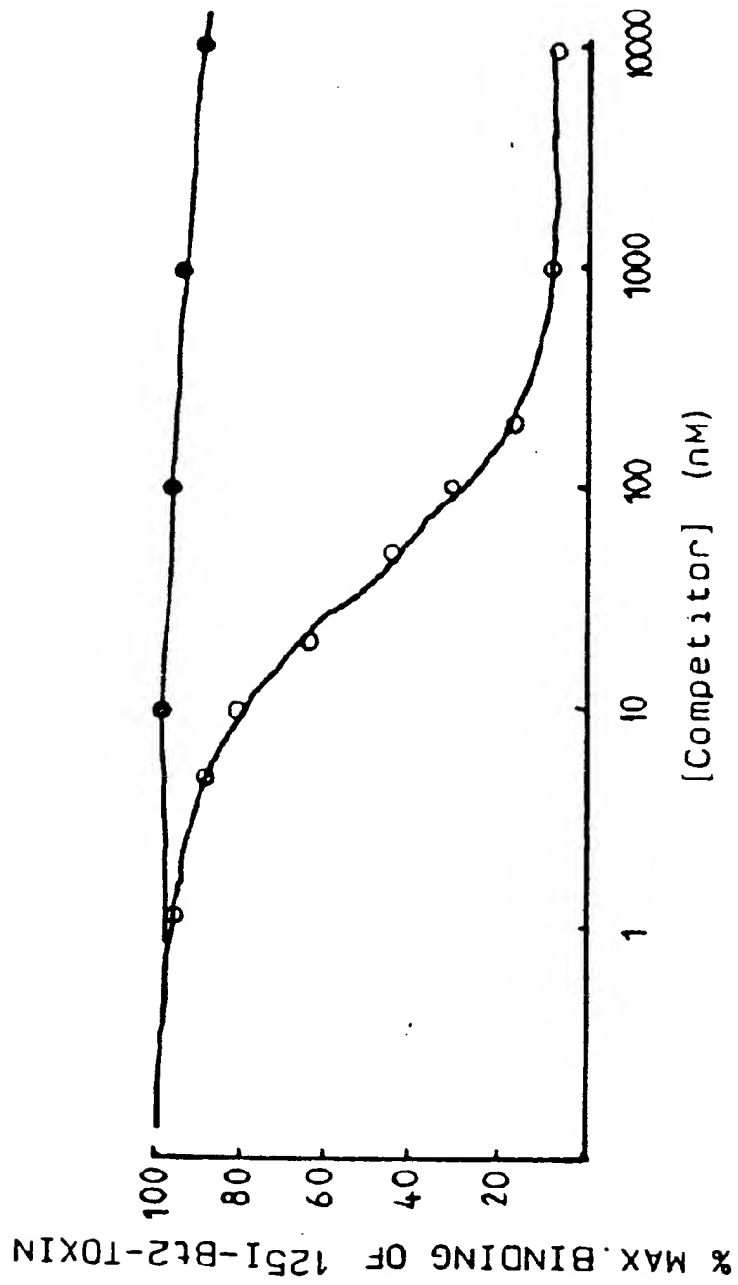


FIGURE 12

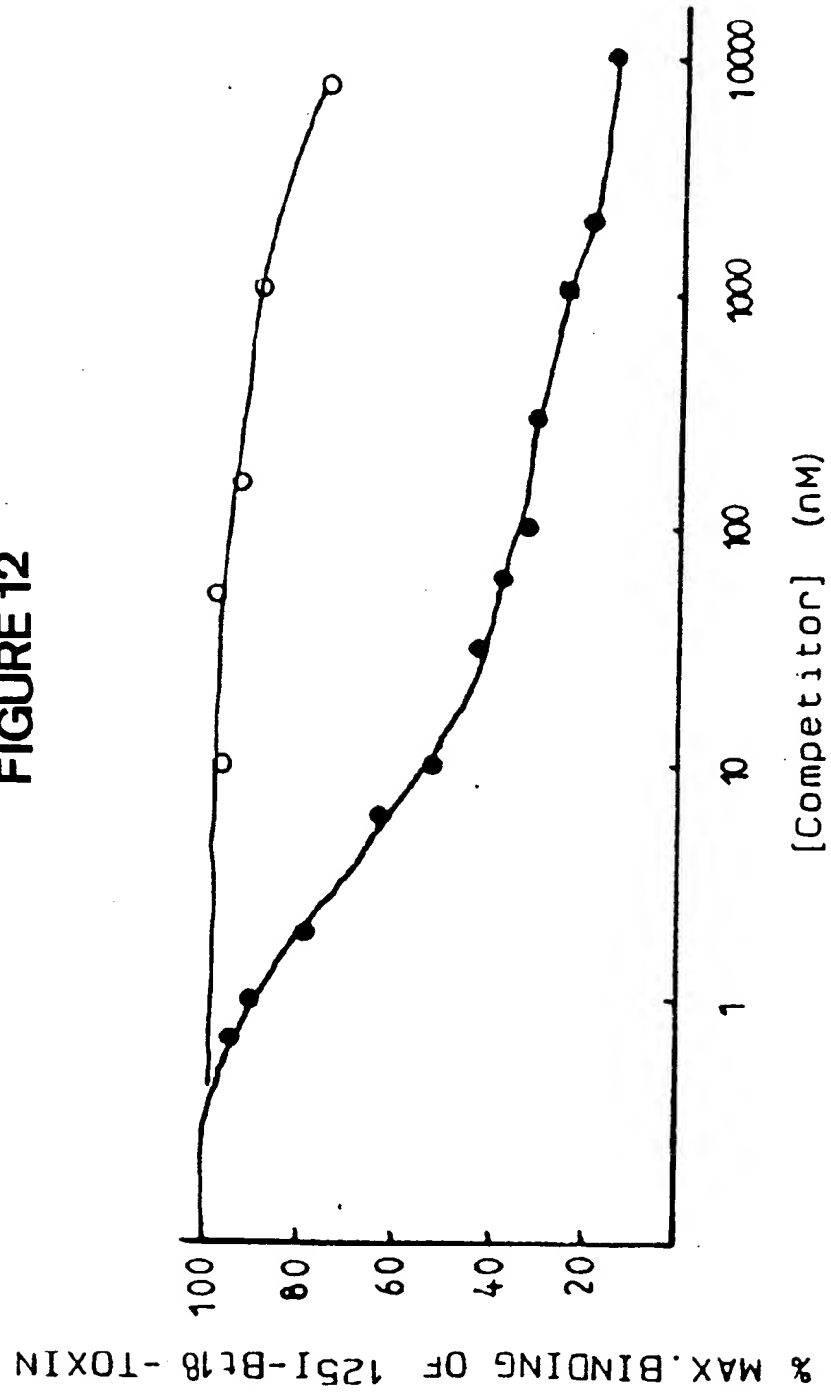


Figure 13

10	20	30	40	50
GGATCTGTTT TAATATAAGG GATTTGTGCC CTTCTCGTTA TATTCTTTTA				
60	70	80	90	100
TTAGCCCCAA AACTAGTGC AACTAAATAT TTTTATAATT AACTGATTA				
110	120	130	140	150
AATACTTTAT TTTTGGGAGT AAGATTTATG CTGAAATGTA ATAAAATTCTG				
160	170	180	190	200
TTCCATTTTC TGTATTTTCT CATAAAATGT TTCATATGCT TTAAATTGTA				
210	220	230	240	250
GTAAAGAAAA ACAGTACAAA CTTAAAAGGA CTTTAGTAAT TTAATAAAAA				
260	269	278	287	
AAGGGGATAG TTT ATG GAA ATA AAT AAT CAA AAC CAA TGT				
MET Glu Ile Asn Asn Gln Asn Gln Cys				

Figure 13 (Cont. 1)

296	305	314	323	
GTG CCT TAC AAT TGT TTA AGT AAT CCT AAG GAG ATA ATA				
Val Pro Tyr Asn Cys Leu Ser Asn Pro Lys Glu Ile Ile				
332	341	350	359	368
TTA GGC GAG GAA AGG CTA GAA ACA GGG AAT ACT GTA GCA				
Leu Gly Glu Glu Arg Leu Glu Thr Gly Asn Thr Val Ala				
377	386	395	404	
GAC ATT TCA TTA GGG CTT ATT AAT TTT CTA TAT TCT AAT				
Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser Asn				
413	422	431	440	
TTT GTA CCA GGA GGA GGA TTT ATA GTA GGT TTA CTA GAA				
Phe Val Pro Gly Gly Gly Phe Ile Val Gly Leu Leu Glu				
449	458	467	476	485
TTA ATA TGG GGA TTT ATA GGG CCT TCG CAA TGG GAT ATT				
Leu Ile Trp Gly Phe Ile Gly Pro Ser Gln Trp Asp Ile				
494	503	512	521	
TTT TTA GCT CAA ATT GAG CAA TTG ATT AGT CAA AGA ATA				
Phe Leu Ala Gln Ile Glu Gln Leu Ile Ser Gln Arg Ile				

Figure 13 (Cont. 2)

530 539 548 557
 GAA GAA TTT GCT AGG AAT CAG GCA ATT TCA AGA TTG GAG
 Glu Glu Phe Ala Arg Asn Gln Ala Ile Ser Arg Leu Glu

566 575 584 593 602
 GGG CTA AGC AAT CTT TAT AAG GTC TAT GTT AGA GCG TTT
 Gly Leu Ser Asn Leu Tyr Lys Val Tyr Val Arg Ala Phe

611 620 629 638
 AGC GAC TGG GAG AAA GAT CCT ACT AAT CCT GCT TTA AGG
 Ser Asp Trp Glu Lys Asp Pro Thr Asn Pro Ala Leu Arg

647 656 665 674
 GAA GAA ATG CGT ATA CAA TTT AAT GAC ATG AAT AGT GCT
 Glu Glu MET Arg Ile Gln Phe Asn Asp MET Asn Ser Ala

683 692 701 710 719
 CTC ATA ACG GCT ATT CCA CTT TTT AGA GTT CAA AAT TAT
 Leu Ile Thr Ala Ile Pro Leu Phe Arg Val Gln Asn Tyr

728 737 746 755
 GAA GTT GCT CTT TTA TCT GTA TAT GTT CAA GCC GCA AAC
 Glu Val Ala Leu Leu Ser Val Tyr Val Gln Ala Ala Asn

Figure 13 (Cont. 3)

764	773	782	791	
TTA CAT TTA TCT ATT TTA AGG GAT GTT TCA GTT TTC GGA				
Leu His Leu Ser Ile Leu Arg Asp Val Ser Val Phe Gly				
800	809	818	827	836
GAA AGA TGG GGA TAT GAT ACA GCG ACT ATC AAT AAT CGC				
Glu Arg Trp Gly Tyr Asp Thr Ala Thr Ile Asn Asn Arg				
845	854	863	872	
TAT AGT GAT CTG ACT AGC CTT ATT CAT GTT TAT ACT AAC				
Tyr Ser Asp Leu Thr Ser Leu Ile His Val Tyr Thr Asn				
881	890	899	908	
CAT TGT GTG GAT ACG TAT AAT CAG GGA TTA AGG CGT TTG				
His Cys Val Asp Thr Tyr Asn Gln Gly Leu Arg Arg Leu				
917	926	935	944	953
GAA GGT CGT TTT CTT AGC GAT TGG ATT GTA TAT AAT CGT				
Glu Gly Arg Phe Leu Ser Asp Trp Ile Val Tyr Asn Arg				
962	971	980	989	
TTC CGG AGA CAA TTG ACA ATT TCA GTA TTA GAT ATT GTT				
Phe Arg Arg Gln Leu Thr Ile Ser Val Leu Asp Ile Val				

Figure 13 (Cont. 4)

998	1007	1016	1025	
GCG TTT TTT CCA AAT TAT GAT ATT AGA ACA TAT CCA ATT				
Ala Phe Phe Pro Asn Tyr Asp Ile Arg Thr Tyr Pro Ile				
1034	1043	1052	1061	1070
CAA ACA GCT ACT CAG CTA ACG AGG GAA GTC TAT CTG GAT				
Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp				
1079	1088	1097	1106	
TTA CCT TTT ATT AAT GAA AAT CTT TCT CCT GCA GCA AGC				
Leu Pro Phe Ile Asn Glu Asn Leu Ser Pro Ala Ala Ser				
1115	1124	1133	1142	
TAT CCA ACC TTT TCA GCT GCT GAA AGT GCT ATA ATT AGA				
Tyr Pro Thr Phe Ser Ala Ala Glu Ser Ala Ile Ile Arg				
1151	1160	1169	1178	1187
AGT CCT CAT TTA GTA GAC TTT TTA AAT AGC TTT ACC ATT				
Ser Pro His Leu Val Asp Phe Leu Asn Ser Phe Thr Ile				
1196	1205	1214	1223	
TAT ACA GAT AGT CTG GCA CGT TAT GCA TAT TGG GGA GGG				
Tyr Thr Asp Ser Leu Ala Arg Tyr Ala Tyr Trp Gly Gly				

Figure 13 (Cont. 5)

1232	1241	1250	1259	
CAC TTG GTA AAT TCT TTC CGC ACA GGA ACC ACT ACT AAT				
His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn				
1268	1277	1286	1295	1304
TTG ATA AGA TCC CCT TTA TAT GGA AGG GAA GGA AAT ACA				
Leu Ile Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr				
1313	1322	1331	1340	
GAG CGC CCC GTA ACT ATT ACC GCA TCA CCT AGC GTA CCA				
Glu Arg Pro Val Thr Ile Thr Ala Ser Pro Ser Val Pro				
1349	1358	1367	1376	
ATA TTT AGA ACA CTT TCA TAT ATT ACA GGC CTT GAC AAT				
Ile Phe Arg Thr Leu Ser Tyr Ile Thr Gly Leu Asp Asn				
1385	1394	1403	1412	1421
TCA AAT CCT GTA GCT GGA ATC GAG GGA GTG GAA TTC CAA				
Ser Asn Pro Val Ala Gly Ile Glu Gly Val Glu Phe Gln				
1430	1439	1448	1457	
AAT ACT ATA AGT AGA AGT ATC TAT CGT AAA AGC GGT CCA				
Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro				

Figure 13 (Cont. 6)

1466	1475	1484	1493	
ATA GAT TCT TTT AGT GAA TTA CCA CCT CAA GAT GCC AGC				
Ile Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser				
1502	1511	1520	1529	1538
GTA TCT CCT GCA ATT GGG TAT AGT CAC CGT TTA TGC CAT				
Val Ser Pro Ala Ile Gly Tyr Ser His Arg Leu Cys His				
1547	1556	1565	1574	
GCA ACA TTT TTA GAA CGG ATT AGT GGA CCA AGA ATA GCA				
Ala Thr Phe Leu Glu Arg Ile Ser Gly Pro Arg Ile Ala				
1583	1592	1601	1610	
GGC ACC GTA TTT TCT TGG ACA CAC CGT AGT GCC AGC CCT				
Gly Thr Val Phe Ser Trp Thr His Arg Ser Ala Ser Pro				
1619	1628	1637	1646	1655
ACT AAT GAA GTA AGT CCA TCT AGA ATT ACA CAA ATT CCA				
Thr Asn Glu Val Ser Pro Ser Arg Ile Thr Gln Ile Pro				
1664	1673	1682	1691	
TGG GTA AAG GCG CAT ACT CTT GCA TCT GGT GCC TCC GTC				
Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val				

Figure 13 (Cont. 7)

1700	1709	1718	1727	
ATT AAA GGT CCT GGA TTT ACA GGT GGA GAT ATT CTG ACT				
Ile Lys Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Thr				
1736	1745	1754	1763	1772
AGG AAT AGT ATG GGC GAG CTG GGG ACC TTA CGA GTA ACC				
Arg Asn Ser MET Gly Glu Leu Gly Thr Leu Arg Val Thr				
1781	1790	1799	1808	
TTC ACA GGA AGA TTA CCA CAA AGT TAT TAT ATA CGT TTC				
Phe Thr Gly Arg Leu Pro Gln Ser Tyr Tyr Ile Arg Phe				
1817	1826	1835	1844	
CGT TAT GCT TCG GTA GCA AAT AGG AGT GGT ACA TTT AGA				
Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr Phe Arg				
1853	1862	1871	1880	1889
TAT TCA CAG CCA CCT TCG TAT GGA ATT TCA TTT CCA AAA				
Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys				
1898	1907	1916	1925	
ACT ATG GAC GCA GGT GAA CCA CTA ACA TCT CGT TCG TTC				
Thr MET Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe				

Figure 13 (Cont. 8)

1934	1943	1952	1961	
GCT CAT ACA ACA CTC TTC ACT CCA ATA ACC TTT TCA CGA				
Ala His Thr Thr Leu Phe Thr Pro Ile Thr Phe Ser Arg				
1970	1979	1988	1997	2006
GCT CAA GAA GAA TTT GAT CTA TAC ATC CAA TCG GGT GTT				
Ala Gln Glu Glu Phe Asp Leu Tyr Ile Gln Ser Gly Val				

2015	2024	2033	2042	
TAT ATA GAT CGA ATT GAA TTT ATA CCG GTT ACT GCA ACA				
Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Thr Ala Thr				
----->				
2051	2060	2069	2078	
TTT GAG GCA GAA TAT GAT TTA GAA AGA GCG CAA AAG GTG				
Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Val				
2087	2096	2105	2114	2123
GTG AAT GCC CTG TTT ACG TCT ACA AAC CAA CTA GGG CTA				
Val Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly Leu				
2132	2141	2150	2159	
AAA ACA GAT GTG ACG GAT TAT CAT ATT GAT CAG GTA TCC				
Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser				

Figure 13 (Cont. 9)

2168	2177	2186	2195	
AAT CTA GTT GCG TGT TTA TCG GAT GAA TTT TGT CTG GAT				
Asn Leu Val Ala Cys Leu Ser Asp Glu Phe Cys Leu Asp				
2204	2213	2222	2231	2240
GAA AAG AGA GAA TTG TCC GAG AAA GTT AAA CAT GCA AAG				
Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys				
2249	2258	2267	2276	
CGA CTC AGT GAT GAG CGG AAT TTA CTT CAA GAT CCA AAC				
Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn				
2285	2294	2303	2312	
TTC AGA GGG ATC AAT AGG CAA CCA GAC CGT GGC TGG AGA				
Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg				
2321	2330	2339	2348	2357
GGA AGT ACG GAT ATT ACT ATC CAA GGA GGA GAT GAC GTA				
Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val				
2366	2375	2384	2393	
TTC AAA GAG AAT TAC GTT ACG CTA CCG GGT ACC TTT GAT				
Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asp				

Figure 13 (Cont. 10)

2402	2411	2420	2429	
GAG TGC TAT CCA ACG TAT TTA TAT CAA AAA ATA GAT GAG				
Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu				
2438	2447	2456	2465	2474
TCG AAA TTA AAA GCC TAT ACC CGT TAT CAA TTA AGA GGG				
Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg Gly				
2483	2492	2501	2510	
TAT ATC GAA GAT AGT CAA GAC TTA GAA ATC TAT TTA ATT				
Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile				
2519	2528	2537	2546	
CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT GTA CCA GGT				
Arg Tyr Asn Ala Lys His Glu Ile Val Asn Val Pro Gly				
2555	2564	2573	2582	2591
ACA GGA AGT TTA TGG CCT CTT TCT GTA GAA AAT CAA ATT				
Thr Gly Ser Leu Trp Pro Leu Ser Val Glu Asn Gln Ile				
2600	2609	2618	2627	
GGA CCT TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT				
Gly Pro Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu				

Figure 13 (Cont. 11)

2636	2645	2654	2663	
GAA TGG AAT CCT GAT TTA CAC TGT TCC TGC AGA GAC GGG				
Glu Trp Asn Pro Asp Leu His Cys Ser Cys Arg Asp Gly				
2672	2681	2690	2699	2708
GAA AAA TGT GCA CAT CAT TCT CAT CAT TTC TCT TTG GAC				
Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp				
2717	2726	2735	2744	
ATT GAT GTT GGA TGT ACA GAC TTA AAT GAG GAC TTA GGT				
Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly				
2753	2762	2771	2780	
GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC CAC				
Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His				
2789	2798	2807	2816	2825
GCA CGA CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA				
Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro				
2834	2843	2852	2861	
TTA TTA GGA GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG				
Leu Leu Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu				

Figure 13 (Cont. 12)

2870.	2879	2888	2897	
AAA AAA TGG AGA GAC AAA CGC GAA ACA TTA CAA TTG GAA				
Lys Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu Glu				
2906	2915	2924	2933	2942
ACA ACT ATC GTT TAT AAA GAG GCA AAA GAA TCT GTA GAT				
Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp				
2951	2960	2969	2978	
GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG				
Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala				
2987	2996	3005	3014	
GAT ACG AAC ATC GCG ATG ATT CAT GCG GCA GAT AAA CGC				
Asp Thr Asn Ile Ala MET Ile His Ala Ala Asp Lys Arg				
3023	3032	3041	3050	3059
GTT CAT AGA ATT CGA GAA GCG TAT CTG CCG GAG CTG TCT				
Val His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser				
3068	3077	3086	3095	
GTG ATT CCG GGT GTC AAT GCG GCT ATT TTT GAA GAA TTA				
Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu Leu				

Figure 13 (Cont. 14)

3338	3347	3356	3365	
TAT GGA GAA GGT TGC GTA ACG ATC CAT GAG ATC GAG AAC				
Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn				
3374	3383	3392	3401	3410
AAT ACA GAC GAA CTG AAA TTC AAC AAC TGT GTA GAA GAG				
Asn Thr Asp Glu Leu Lys Phe Asn Asn Cys Val Glu Glu				
3419	3428	3437	3446	
GAA GTA TAT CCA AAC AAC ACG GTA ACG TGT ATT AAT TAT				
Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Ile Asn Tyr				
3455	3464	3473	3482	
ACT GCG ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT				
Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser				
3491	3500	3509	3518	3527
CGT AAT CGA GGA TAT GAC GAA GCC TAT GGT AAT AAC CCT				
Arg Asn Arg Gly Tyr Asp Glu Ala Tyr Gly Asn Asn Pro				
3536	3545	3554	3563	
TCC GTA CCA GCT GAT TAT GCG TCA GTC TAT GAA GAA AAA				
Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys				

Figure 13 (Cont. 13)

3104	3113	3122	3131	
GAA GAG CGT ATT TTC ACT GCA TTT TCC CTA TAT GAT GCG				
Glu Glu Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala				
3140	3149	3158	3167	3176
AGA AAT ATT ATT AAA AAT GGC GAT TTC AAT AAT GGC TTA				
Arg Asn Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu				
3185	3194	3203	3212	
TTA TGC TGG AAC GTG AAA GGG CAT GTA GAG GTA GAA GAA				
Leu Cys Trp Asn Val Lys Gly His Val Glu Val Glu Glu				
3221	3230	3239	3248	
CAA AAC AAT CAC CGT TCA GTC CTG GTT ATC CCA GAA TGG				
Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp				
3257	3266	3275	3284	3293
GAG GCA GAA GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT				
Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly				
3302	3311	3320	3329	
CGT GGC TAT ATC CTT CGT GTT ACA GCG TAC AAA GAG GGA				
Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly				

Figure 13 (Cont. 15)

3572	3581	3590	3599	
TCG TAT ACA GAT AGA CGA AGA GAG AAT CCT TGT GAA TCT				
Ser Tyr Thr Asp Arg Arg Arg Glu Asn Pro Cys Glu Ser				
3608	3617	3626	3635	3644
AAC AGA GGA TAT GGA GAT TAC ACA CCA CTA CCA GCT GGT				
Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly				
3653	3662	3671	3680	
TAT GTA ACA AAG GAA TTA GAG TAC TTC CCA GAG ACC GAT				
Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp				
3689	3698	3707	3716	
AAG GTA TGG ATT GAG ATT GGA GAA ACA GAA GGA ACA TTC				
Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe				
3725	3734	3743	3752	3761
ATC GTG GAC AGC GTG GAA TTA CTC CTT ATG GAG GAA TAG				
Ile Val Asp Ser Val Glu Leu Leu Leu MET Glu Glu .				

Figure 13 (Cont. 16)

3771 3781 3791 3801 3811
GACCATCCGA GTATAGCAGT TTAATAAATA TTAATTAAAA TAGTAGTCTA

3821 3831 3841 3851 3861
ACTTCCGTTC CAATTAAATA AGTAAATTAC AGTTGTAAAA AAAAACGAAC

3871 3881 3891 3901
ATTACTCTTC AAAGAGCGAT GTCCGTTTTT TATATGGTGT GT

Figure 14

10	20	30	40	50
AATAGAATCT	CAAATCTCGA	TGACTGCTTA	GTCTTTTAA	TACTGTCTAC
60	70	80	90	100
TTGACAGGGG	TAGGAACATA	ATCGGTCAAT	TTTAAATATG	GGGCATATAT
110	120	130	140	150
TGATATTTTA	TAAAATTTGT	TACGTTTTTT	GTATTTTTTC	ATAAGATCTG
160	170	180	190	200
TCATATGTAT	TAAATCGTGG	TAATGAAAAA	CAGTATCAAA	CTATCAGAAC
210	220	230	239	
TTTGGTAGTT	TAATAAAAAA	ACGGAGGTAT	TTT ATG GAG GAA	
		-----	MET Glu Glu	
248	257	266	275	
AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT				
Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser				
284	293	302	311	320
AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA				
Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser				

Figure 14 (Cont. 1)

329 338 347 356
ACT GGT AAT TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT
Thr Gly Asn Ser Ser Ile Asp Ile Ser Leu Ser Leu Val

365 374 383 392
CAG TTT CTG GTA TCT AAC TTT GTA CCA GGG GGA GGA TTT
Gln Phe Leu Val Ser Asn Phe Val Pro Gly Gly Gly Phe

401 410 419 428 437
TTA GTT GGA TTA ATA GAT TTT GTA TGG GGA ATA GTT GGC
Leu Val Gly Leu Ile Asp Phe Val Trp Gly Ile Val Gly

446 455 464 473
CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA CAA
Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu Gln

482 491 500 509
TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT
Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala

518 527 536 545 554
GCT ATT GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT
Ala Ile Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn

Figure 14 (Cont. 2)

563	572	581	590	
ATA TAT GTG GAA GCA	TTT AAA GAA TGG	GAA GAA GAT	CCT	
Ile Tyr Val Glu Ala	Phe Lys Glu Trp	Glu Glu Asp	Pro	
599	608	617	626	
AAT AAT CCA GAA ACC	AGG ACC AGA GTA	ATT GAT CGC	TTT	
Asn Asn Pro Glu Thr	Arg Thr Arg Val	Ile Asp Arg	Phe	
635	644	653	662	671
CGT ATA CTT GAT GGG	CTA CTT GAA AGG	GAC ATT CCT	TCG	
Arg Ile Leu Asp Gly	Leu Leu Glu Arg	Asp Ile Pro	Ser	
680	689	698	707	
TTT CGA ATT TCT GGA	TTT GAA GTA CCC	CTT TTA TCC	GTT	
Phe Arg Ile Ser Gly	Phe Glu Val Pro	Leu Leu Ser	Val	
716	725	734	743	
TAT GCT CAA GCG GCC	AAT CTG CAT CTA	GCT ATA TTA	AGA	
Tyr Ala Gln Ala Ala	Asn Leu His Leu	Ala Ile Leu	Arg	
752	761	770	779	788
GAT TCT GTA ATT TTT	GGA GAA AGA TGG	GGA TTG ACA	ACG	
Asp Ser Val Ile Phe	Gly Glu Arg Trp	Gly Leu Thr	Thr	

Figure 14 (Cont. 3)

797	806	815	824
ATA AAT GTC AAT GAA AAC TAT AAT AGA CTA ATT AGG CAT			
Ile Asn Val Asn Glu Asn Tyr Asn Arg Leu Ile Arg His			

833	842	851	860
ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT ACG TAT AAT			
Ile Asp Glu Tyr Ala Asp His Cys Ala Asn Thr Tyr Asn			

869	878	887	896	905
CGG GGA TTA AAT AAT TTA CCG AAA TCT ACG TAT CAA GAT				
Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp				

914	923	932	941
TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG			
Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu			

950	959	968	977
ACT GTA TTA GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC			
Thr Val Leu Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp			

986	995	1004	1013	1022
AAT AGG AGA TAT CCA ATT CAG CCA GTT GGT CAA CTA ACA				
Asn Arg Arg Tyr Pro Ile Gln Pro Val Gly Gln Leu Thr				

Figure 14 (Cont. 4)

1031	1040	1049	1058	
AGG GAA GTT TAT ACG GAC CCA TTA ATT AAT TTT AAT CCA				
Arg Glu Val Tyr Thr Asp Pro Leu Ile Asn Phe Asn Pro				
1067	1076	1085	1094	
CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC GTT				
Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn Val				
1103	1112	1121	1130	1139
ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT				
MET Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp				
1148	1157	1166	1175	
ATA TTG AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT				
Ile Leu Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser				
1184	1193	1202	1211	
GTT GGA CGC AAT TTT TAT TGG GGA GGA CAT CGA GTA ATA				
Val Gly Arg Asn Phe Tyr Trp Gly Gly His Arg Val Ile				
1220	1229	1238	1247	1256
TCT AGC CTT ATA GGA GGT GGT AAC ATA ACA TCT CCT ATA				
Ser Ser Leu Ile Gly Gly Gly Asn Ile Thr Ser Pro Ile				

Figure 14 (Cont. 5)

1265	1274	1283	1292	
TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA TCC TTT				
Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg Ser Phe				
1301	1310	1319	1328	
ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT				
Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro				
1337	1346	1355	1364	1373
ACT TTA CGA TTA TTA CAG CAA CCT TGG CCA GCG CCA CCA				
Thr Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro				
1382	1391	1400	1409	
TTT AAT TTA CGT GGT GTT GAA GGA GTA GAA TTT TCT ACA				
Phe Asn Leu Arg Gly Val Glu Gly Val Glu Phe Ser Thr				
1418	1427	1436	1445	
CCT ACA AAT AGC TTT ACG TAT CGA GGA AGA GGT ACG GTT				
Pro Thr Asn Ser Phe Thr Tyr Arg Gly Arg Gly Thr Val				
1454	1463	1472	1481	1490
GAT TCT TTA ACT GAA TTA CCG CCT GAG GAT AAT AGT GTG				
Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp Asn Ser Val				

Figure 14 (Cont. 6)

1499	1508	1517	1526	
CCA CCT CGC GAA GGA TAT AGT CAT CGT TTA TGT CAT GCA				
Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala				
1535	1544	1553	1562	
ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT				
Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr				
1571	1580	1589	1598	1607
GGT GTA GTA TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT				
Gly Val Val Phe Ser Trp Thr His Arg Ser Ala Thr Leu				
1616	1625	1634	1643	
ACA AAT ACA ATT GAT CCA GAG AGA ATT AAT CAA ATA CCT				
Thr Asn Thr Ile Asp Pro Glu Arg Ile Asn Gln Ile Pro				
1652	1661	1670	1679	
TTA GTG AAA GGA TTT AGA GTT TGG GGG GGC ACC TCT GTC				
Leu Val Lys Gly Phe Arg Val Trp Gly Gly Thr Ser Val				
1688	1697	1706	1715	1724
ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT CGA				
Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg				

Figure 14 (Cont. 7)

1733	1742	1751	1760	
AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT				
Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn				
1769	1778	1787	1796	
ATT AAT TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT				
Ile Asn Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe				
1805	1814	1823	1832	1841
CGT TAC GCT TCC AGT AGG GAT GCA CGA GTT ATA GTA TTA				
Arg Tyr Ala Ser Ser Arg Asp Ala Arg Val Ile Val Leu				
1850	1859	1868	1877	
ACA GGA GCG GCA TCC ACA GGA GTG GGA GGC CAA GTT AGT				
Thr Gly Ala Ala Ser Thr Gly Val Gly Gly Gln Val Ser				
1886	1895	1904	1913	
GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA GGG GAG				
Val Asn MET Pro Leu Gln Lys Thr MET Glu Ile Gly Glu				
1922	1931	1940	1949	1958
AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT				
Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser				

Figure 14 (Cont. 8)

1967	1976	1985	1994	
AAT CCT TTT TCA	TTT AGA GCT	AAT CCA GAT	ATA ATT GGG	
Asn Pro Phe Ser	Phe Arg Ala Asn	Pro Asp Ile	Ile Gly	
2003	2012	2021	2030	
ATA AGT GAA CAA	CCT CTA TTT	GGT GCA GGT	TCT ATT AGT	
Ile Ser Glu Gln	Pro Leu Phe	Gly Ala Gly	Ser Ile Ser	
2039	2048	2057	2066	2075
AGC GGT GAA CTT	TAT ATA GAT	AAA ATT GAA	ATT ATT CTA	
Ser Gly Glu Leu	Tyr Ile Asp	Lys Ile Glu	Ile Ile Leu	
2084	2093	2102	2111	
GCA GAT GCA ACA	TTT GAA GCA	GAA TCT GAT	TTA GAA AGA	
Ala Asp Ala Thr	Phe Glu Ala	Glu Ser Asp	Leu Glu Arg	
2120	2129	2138	2147	
GCA CAA AAG GCG	GTG AAT GCC	CTG TTT ACT	TCT TCC AAT	
Ala Gln Lys Ala	Val Asn Ala	Leu Phe Thr	Ser Ser Asn	
2156	2165	2174	2183	2192
CAA ATC GGG TTA	AAA ACC GAT	GTG ACG GAT	TAT CAT ATT	
Gln Ile Gly Leu	Lys Thr Asp	Val Thr Asp	Tyr His Ile	

Figure 14 (Cont. 9)

2201	2210	2219	2228	
GAT CAA GTA TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA				
Asp Gln Val Ser Asn Leu Val Asp Cys Leu Ser Asp Glu				
2237	2246	2255	2264	
TTT TGT CTG GAT GAA AAG CGA GAA TTG TCC GAG AAA GTC				
Phe Cys Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val				
2273	2282	2291	2300	2309
AAA CAT GCG AAG CGA CTC AGT GAT GAG CGG AAT TTA CTT				
Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu				
2318	2327	2336	2345	
CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA GAC				
Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro Asp				
2354	2363	2372	2381	
CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA				
Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly				
2390	2399	2408	2417	2426
GGA GAT GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG				
Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro				

Figure 14 (Cont. 10)

2435	2444	2453	2462	
GGT ACC GTT GAT GAG TGC TAT CCA ACG TAT TTA TAT CAG				
Gly Thr Val Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln				
2471	2480	2489	2498	
AAA ATA GAT GAG TCG AAA TTA AAA GCT TAT ACC CGT TAT				
Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr				
2507	2516	2525	2534	2543
GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC TTA GAA				
Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu				
2552	2561	2570	2579	
ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA				
Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val				
2588	2597	2606	2615	
AAT GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC				
Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala				
2624	2633	2642	2651	2660
CAA AGT CCA ATC GGA AAG TGT GGA GAA CCG AAT CGA TGC				
Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys				

Figure 14 (Cont. 11)

2669	2678	2687	2696	
GCG CCA CAC CTT GAA TGG AAT CCT GAT CTA GAT TGT TCC				
Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser				
2705	2714	2723	2732	
TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT TCC CAT CAT				
Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His				
2741	2750	2759	2768	2777
TTC ACC TTG GAT ATT GAT GTT GCA TGT ACA GAC TTA AAT				
Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn				
2786	2795	2804	2813	
GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG				
Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr				
2822	2831	2840	2849	
CAA GAT GGC CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC				
Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu				
2858	2867	2876	2885	2894
GAA GAG AAA CCA TTA TTA GGG GAA GCA CTA GCT CGT GTG				
Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val				

Figure 14 (Cont. 12)

2903	2912	2921	2930	
AAA AGA GCG GAG AAG AAG TGG AGA GAC AAA CGA GAG AAA				
Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys				
2939	2948	2957	2966	
CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA AAA				
Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys				
2975	2984	2993	3002	3011
GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT				
Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp				
3020	3029	3038	3047	
AGA TTA CAA GTG GAT ACG AAC ATC GCG ATG ATT CAT GCG				
Arg Leu Gln Val Asp Thr Asn Ile Ala MET Ile His Ala				
3056	3065	3074	3083	
GCA GAT AAA CGC GTT CAT AGA ATC CGG GAA GCG TAT CTG				
Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu				
3092	3101	3110	3119	3128
CCA GAG TTG TCT GTG ATT CCA GGT GTC AAT GCG GCC ATT				
Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile				

Figure 14 (Cont. 13)

3137	3146	3155	3164	
TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG TAT TCC				
Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Tyr Ser				
3173	3182	3191	3200	
TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC				
Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe				
3209	3218	3227	3236	3245
AAT AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA				
Asn Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val				
3254	3263	3272	3281	
GAT GTA GAA GAG CAA AAC AAC CAC CGT TCG GTC CTT GTT				
Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu Val				
3290	3299	3308	3317	
ATC CCA GAA TGG GAG GCA GAA GTG TCA CAA GAG GTT CGT				
Ile Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg				
3326	3335	3344	3353	3362
GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT GTC ACA GCA				
Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala				

Figure 14 (Cont. 14)

3371	3380	3389	3398	
TAT AAA GAG GGA	TAT GGA GAG GGC	TGC GTA ACG	ATC CAT	
Tyr Lys Glu Gly	Tyr Gly Glu Gly	Cys Val Thr	Ile His	
3407	3416	3425	3434	
GAG ATC GAA GAC	AAT ACA GAC GAA	CTG AAA TTC	AGC AAC	
Glu Ile Glu Asp	Asn Thr Asp Glu	Leu Lys Phe	Ser Asn	
3443	3452	3461	3470	3479
TGT GTA GAA GAG	GAA GTA TAT CCA	AAC AAC ACA	GTA ACG	
Cys Val Glu Glu	Glu Val Tyr Pro	Asn Asn Thr	Val Thr	
3488	3497	3506	3515	
TGT AAT AAT TAT	ACT GGG ACT CAA	GAA GAA TAT	GAG GGT	
Cys Asn Asn Tyr	Thr Gly Thr Gln	Glu Glu Tyr	Glu Gly	
3524	3533	3542	3551	
ACG TAC ACT TCT	CGT AAT CAA GGA	TAT GAC GAA	GCC TAT	
Thr Tyr Thr Ser	Arg Asn Gln Gly	Tyr Asp Glu	Ala Tyr	
3560	3569	3578	3587	3596
GGT AAT AAC CCT	TCC GTA CCA GCT	GAT TAC GCT	TCA GTC	
Gly Asn Asn Pro	Ser Val Pro Ala	Asp Tyr Ala	Ser Val	

Figure 14 (Cont. 15)

3605	3614	3623	3632	
TAT GAA GAA AAA TCG	TAT ACA GAT GGA	CGA AGA GAG AAT		
Tyr Glu Glu Lys Ser	Tyr Thr Asp Gly	Arg Arg Glu Asn		
3641	3650	3659	3668	
CCT TGT GAA TCT AAC	AGA GGC TAT GGG	GAT TAC ACA CCA		
Pro Cys Glu Ser Asn	Arg Gly Tyr Gly	Asp Tyr Thr Pro		
3677	3686	3695	3704	3713
CTA CCG GCT GGT TAT	GTA ACA AAG GAT	TTA GAG TAC TTC		
Leu Pro Ala Gly Tyr	Val Thr Lys Asp	Leu Glu Tyr Phe		
3722	3731	3740	3749	
CCA GAG ACC GAT AAG	GTA TGG ATT GAG	ATC GGA GAA ACA		
Pro Glu Thr Asp Lys	Val Trp Ile Glu	Ile Gly Glu Thr		
3758	3767	3776	3785	
GAA GGA ACA TTC ATC	GTG GAT AGC GTG	GAA TTA CTC CTT		
Glu Gly Thr Phe Ile	Val Asp Ser Val	Glu Leu Leu Leu		
3794	3803	3813	3823	3833
ATG GAG GAA TAA	GATACGTTAT	AAAATGTAAC	GTATGCAAAT	
MET Glu Glu	.			

Figure 14 (Cont. 16)

3843	3853	3863	3873	3883
AAAGAATGAT	TACTGACCTA	TATTAACAGA	TAAATAAGAA	AATTTTATA
3893	3903	3913	3923	
CGAATAAAAA	ACGGACATCA	CTCTTAAGAG	AATGATGTCC	

FIGURE 15

a)

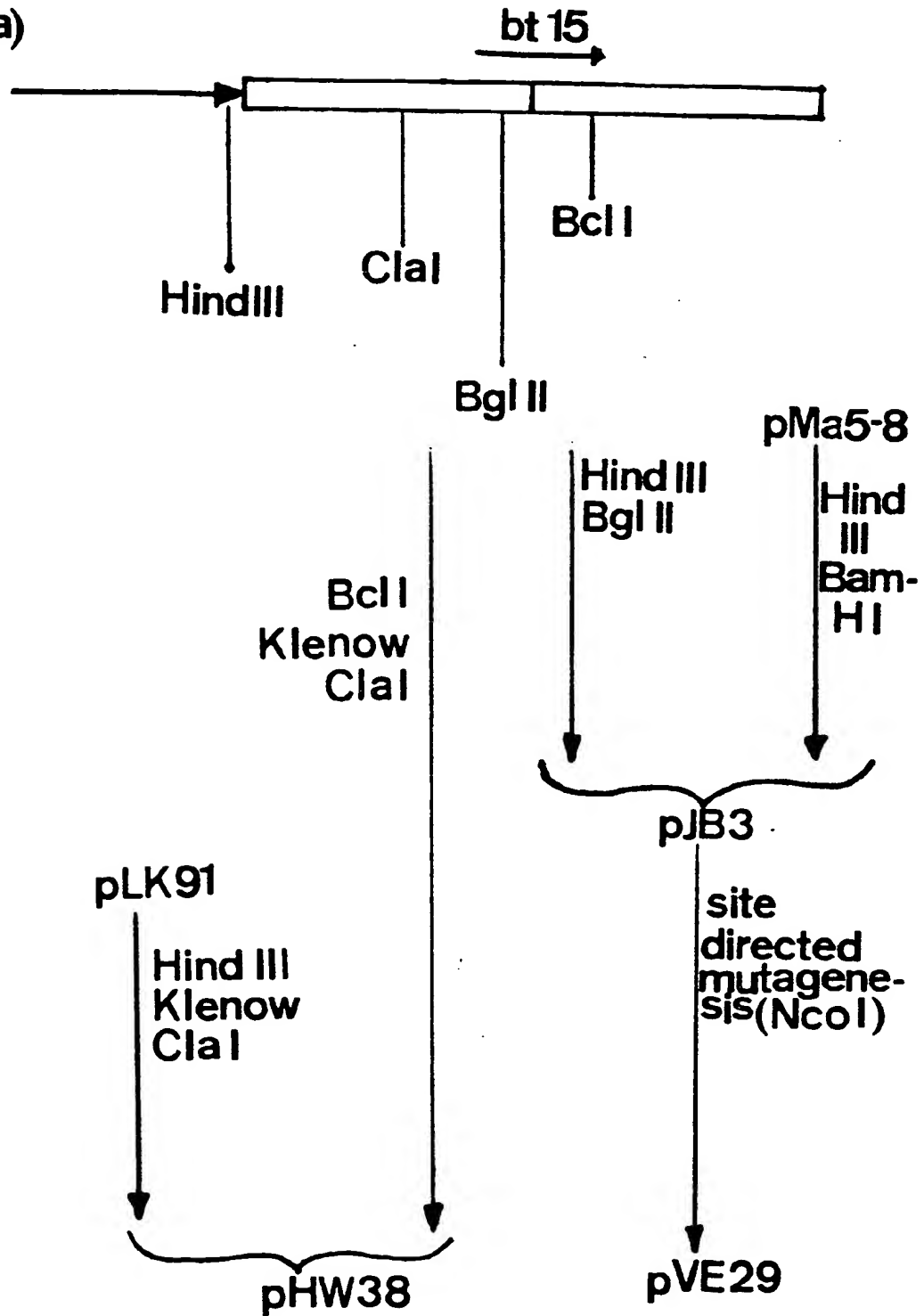
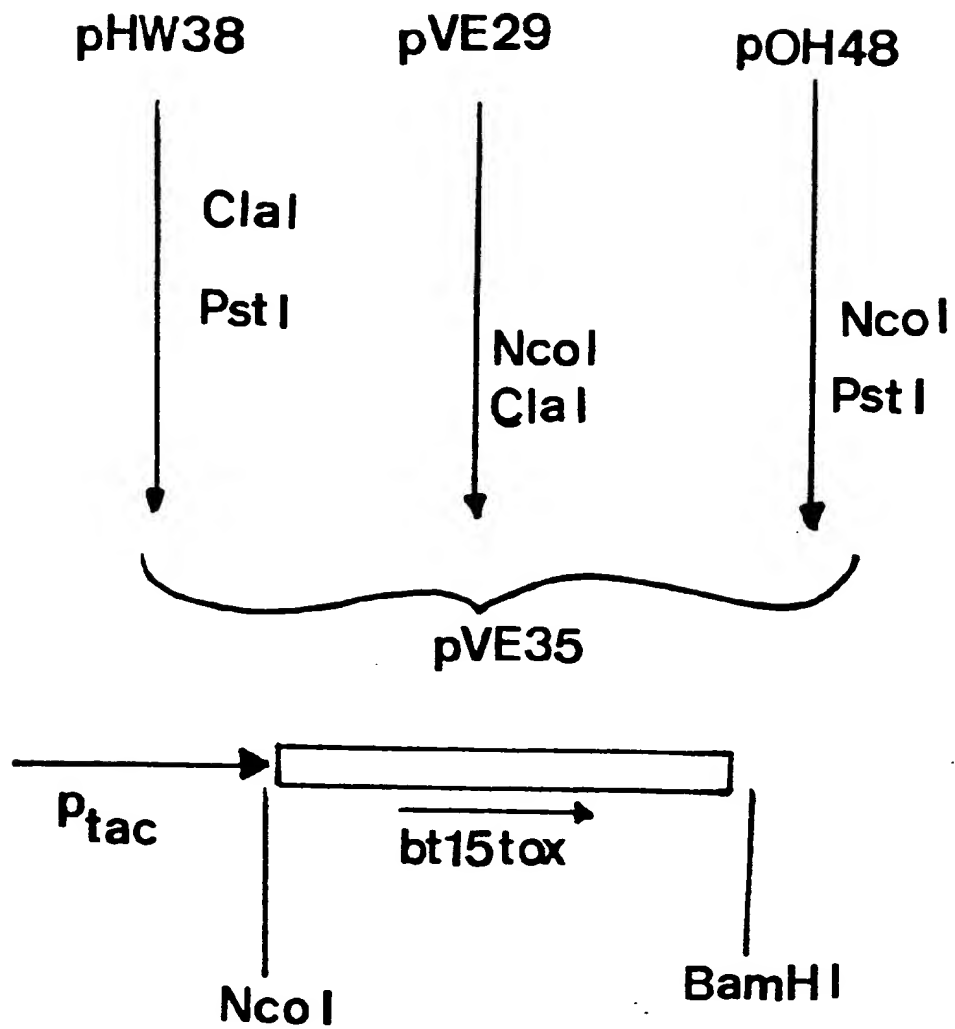


Fig. 15 (cont)

b)



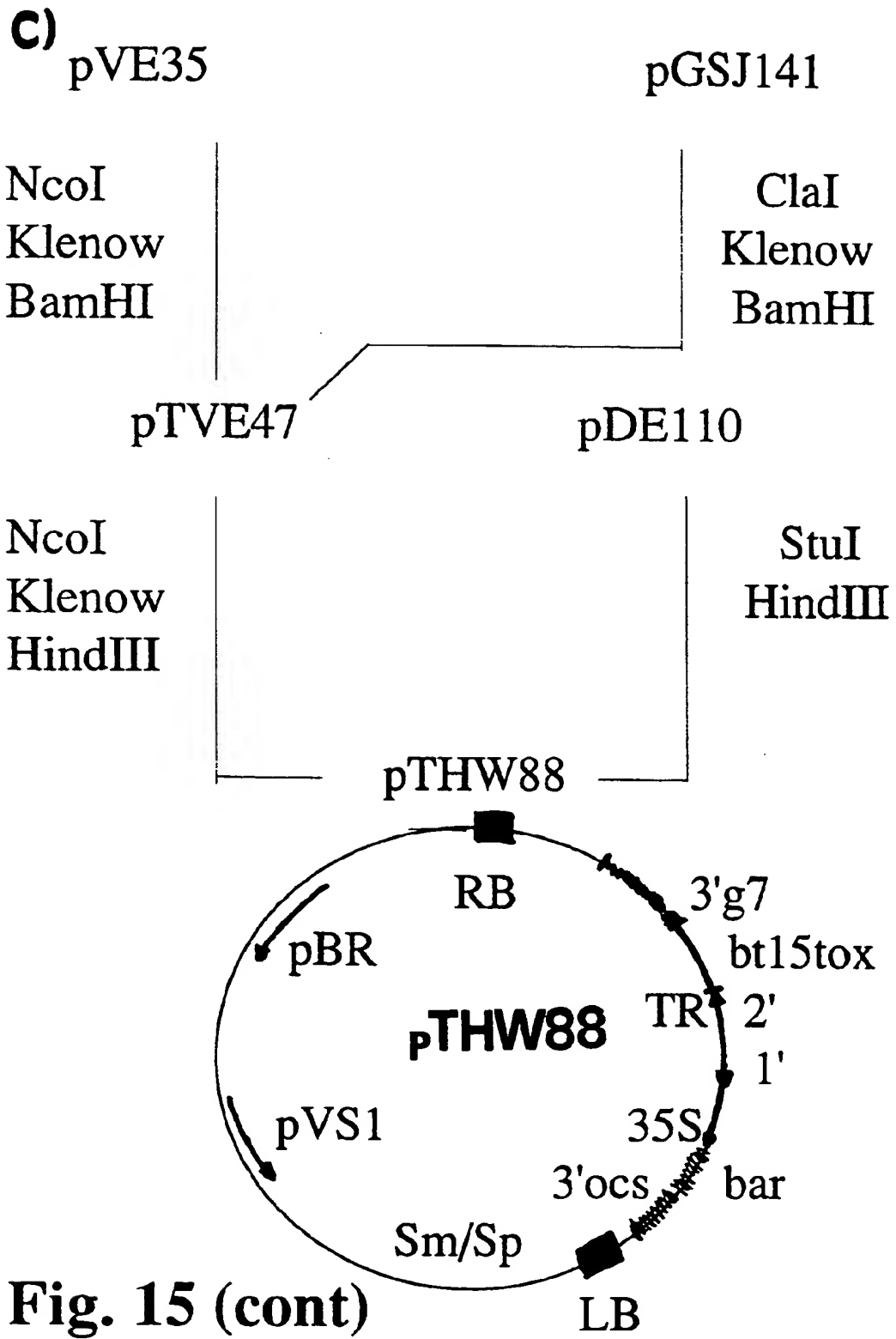


Fig. 15 (cont)

FIGURE 16
a)

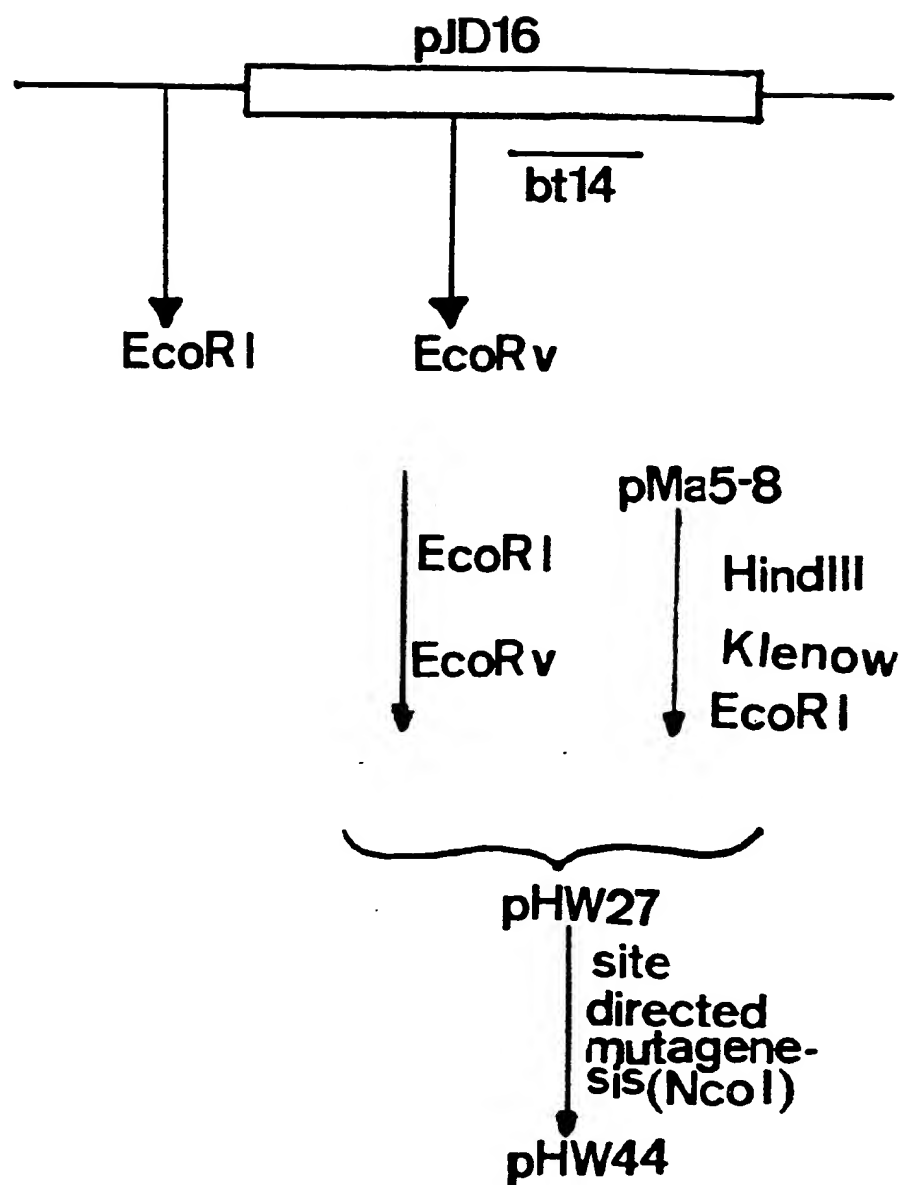


FIGURE 16

b)

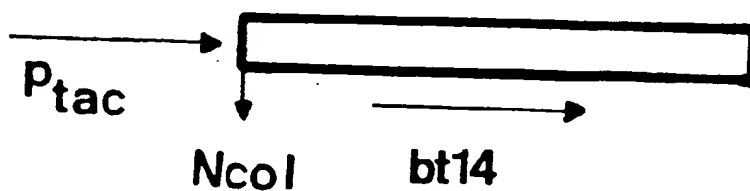
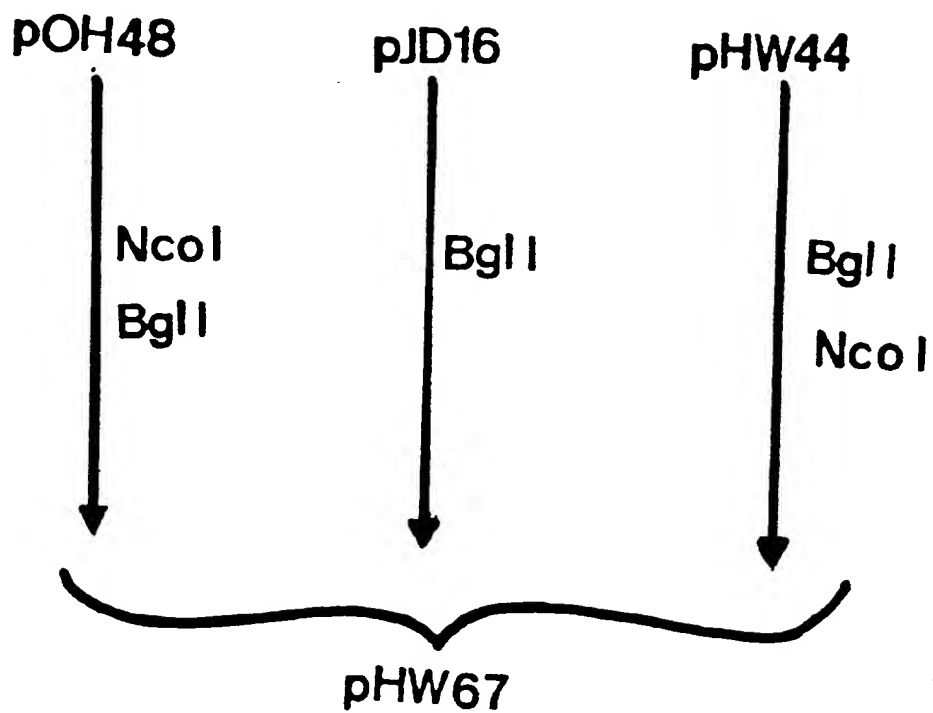


FIGURE 16

c)

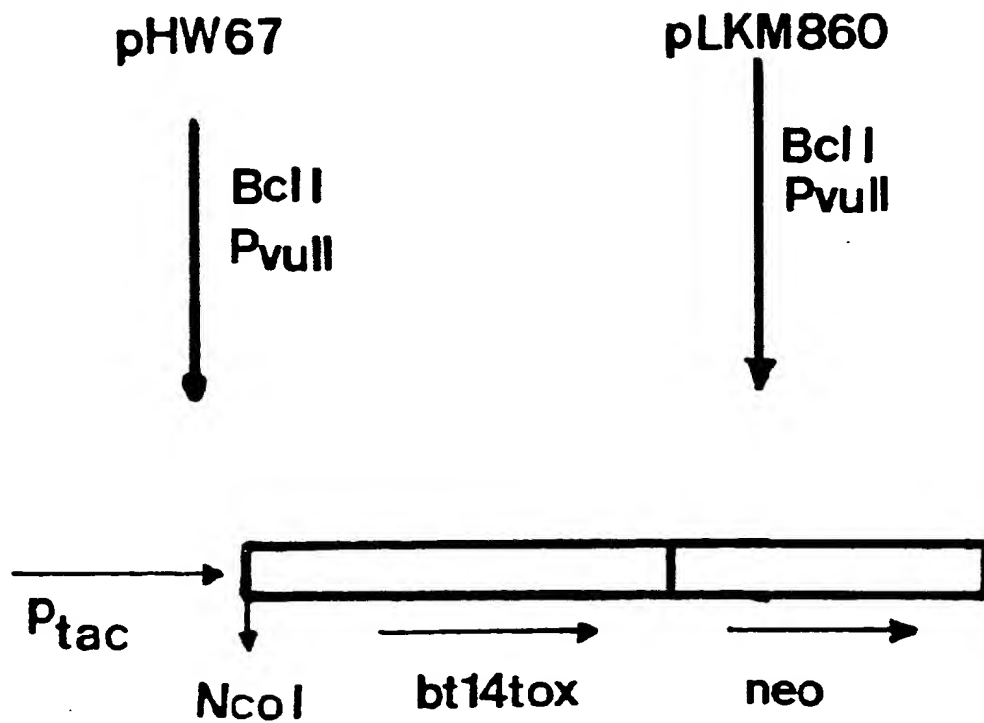


FIGURE 16 (CONT)

d)

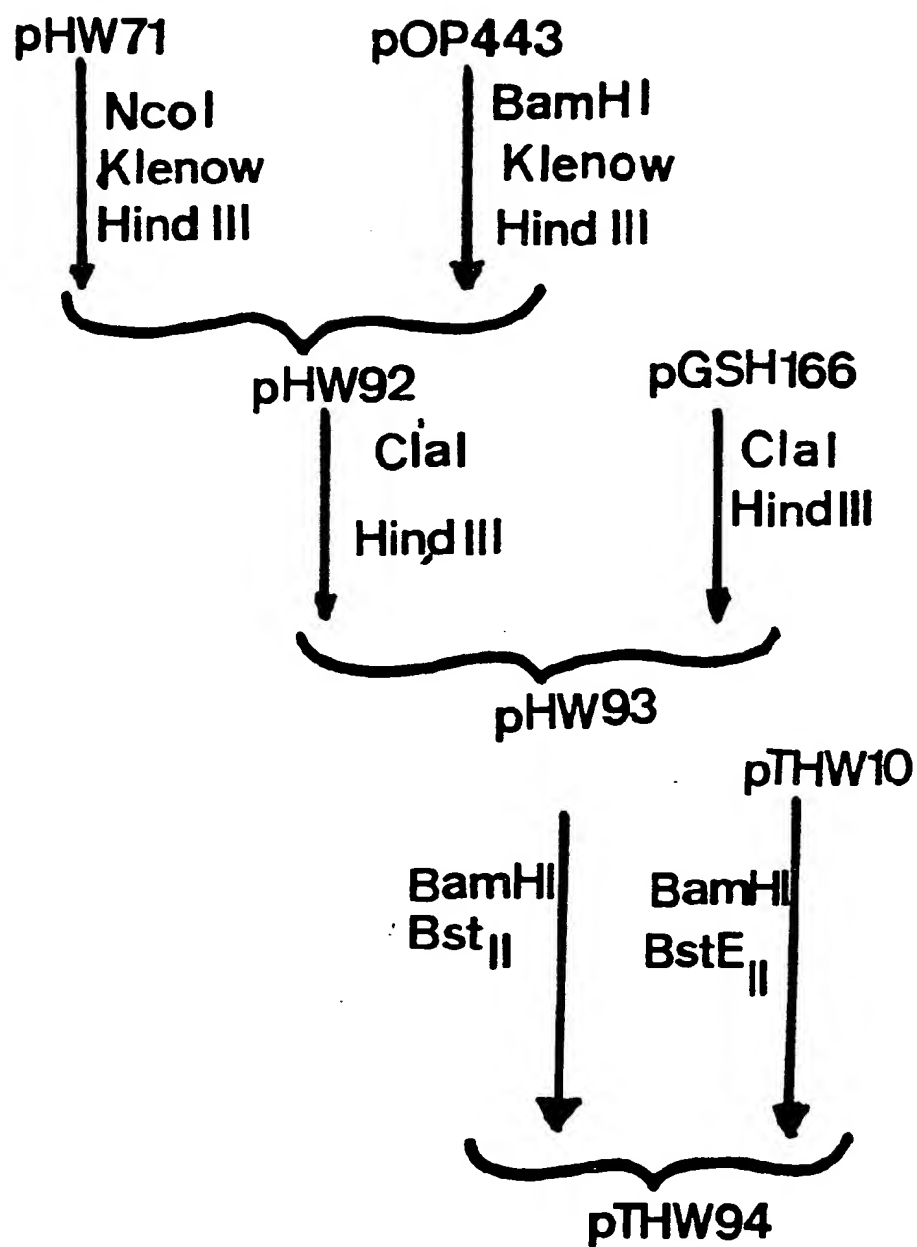


FIGURE 16 (CONT)

